SCORE Search Results Details for Application 10553509 and Search Result 20061214_104100_us-10-553-509-11.szlm60.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104100_us-10-53-509-11.szlm60.rng.

tart | next page

Go Back to previous pag

```
                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


M nucleic - nucleic search, using sw model

un on:          December 15, 2006, 05:57:43 ; Search time 192.899 Seconds
                                            (without alignments)
                                            578.313 Million cell updates/sec

itle:           US-10-553-509-11
erfect score:   16
equence:        1 catcgcctggactccg 16

coring table:   IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

earched:        5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters:      5397982

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase :        N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES

                 %
esult            Query
  No.    Score   Match Length DB  ID                          Description
---------------------------------------------------------------------------
```

	2	16	100.0	17	2	AAT58987	Aat58987 Obesity a
	3	16	100.0	17	14	AEC91758	Aec91758 Probe 5T-
	4	16	100.0	18	13	ADT93450	Adt93450 Fluoresce
	5	16	100.0	19	6	ABK50102	Abk50102 Allele sp
	6	16	100.0	20	13	ADT93449	Adt93449 Fluoresce
	7	16	100.0	21	4	AAF96885	Aaf96885 Human gen
	8	16	100.0	25	12	ADO26525	Ado26525 Novel hyb
	9	16	100.0	26	6	ABL40567	Abl40567 Primer #7
	10	16	100.0	34	13	ADT93453	Adt93453 Human bet
	11	15.6	100.0	21	3	AAC73164	Aac73164 SNP flank
	12	15.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
	13	15.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
	14	15	93.8	15	13	ADT93452	Adt93452 Fluoresce
	15	15	93.8	18	14	AEC91756	Aec91756 Probe 3T-
	16	14.4	90.0	17	2	AAT58988	Aat58988 Obesity a
	17	14.4	90.0	17	2	AAT58990	Aat58990 Obesity a
	18	14.4	90.0	19	13	ADT93446	Adt93446 Fluoresce
	19	14.4	90.0	21	14	AEC91760	Aec91760 Probe 3T-
	20	14.4	90.0	25	6	ABL40568	Abl40568 Primer #8
	21	14.4	90.0	25	12	ADO26526	Ado26526 Novel hyb
	22	14.4	90.0	34	13	ADT93454	Adt93454 Human bet
	23	14.4	90.0	41	6	ABK50104	Abk50104 Sense str
	24	14	87.5	14	13	ADU50896	Adu50896 Human bet
	25	14	87.5	14	14	ADZ42342	Adz42342 FAM probe
	26	14	87.5	21	4	AAF96886	Aaf96886 Human gen
	27	14	87.5	51	4	AAH90342	Aah90342 Human clo
	28	14	87.5	51	4	AAH90341	Aah90341 Human clo
	29	13.6	85.0	34	2	AAV33317	Aav33317 Anti-CD23
	30	13.4	83.8	16	13	ADT93445	Adt93445 Fluoresce
	31	13.4	83.8	25	4	AAC89164	Aac89164 Sample DN
	32	13.4	83.8	33	2	AAQ87254	Aaq87254 Primer fo
	33	13.4	83.8	35	2	AAV24264	Aav24264 Chimeric
	34	13.4	83.8	35	2	AAX00108	Aax00108 Human ant
	35	13.4	83.8	35	3	AAZ58889	Aaz58889 PCR prime
	36	13.4	83.8	35	4	AAF69217	Aaf69217 Chimeric
	37	13.4	83.8	35	4	AAF69105	Aaf69105 Chimeric
	38	13.4	83.8	35	4	AAH75082	Aah75082 Nucleotid
	39	13.4	83.8	35	4	AAH76620	Aah76620 Chimeric
	40	13.4	83.8	35	5	AAH74261	Aah74261 Nucleotid
	41	13.4	83.8	35	5	AAF69161	Aaf69161 Chimeric
	42	13.4	83.8	35	6	ABL94797	Abl94797 Joint dis
	43	13.4	83.8	35	10	ABT31649	Abt31649 Angiogene
	44	13.4	83.8	35	12	ADO33818	Ado33818 Parathyro
	45	13.4	83.8	35	13	ADT93451	Adt93451 Fluoresce

ALIGNMENTS

```
ESULT 1
DT93451
D   ADT93451 standard; DNA; 16 BP.
K
C   ADT93451;
K
R   13-JAN-2005  (first entry)
K
E   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 11.
K
W   SNP detection; beta3 adrenaline receptor; ss; probe.
K
S   Homo sapiens.
K
H   Key             Location/Qualifiers
F   modified_base   1
F                   /*tag=  a
F                   /mod_base= OTHER
F                   /note= "OTHER = Linked to BODIPY FL group"
F   modified_base   16
F                   /*tag=  b
F                   /mod_base= OTHER
```

XX
PN   WO2004092385-A1.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-JP005525.
XX
PR   18-APR-2003; 2003JP-00114381.
XX
PA   (ARKR-) ARKRAY INC.
XX
PI   Hirai M;
XX
DR   WPI; 2004-784610/77.
XX
PT   Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT   receptor gene having single nucleotide polymorphism, labeled at terminal
PT   with fluorescent dye and shows decrease in fluorescence of fluorescent
PT   dye upon hybridization.
XX
PS   Claim 2; SEQ ID NO 11; 31pp; Japanese.
XX
CC   The invention relates to a novel nucleic acid probe which is labelled at
CC   a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC   of the fluorescent dye is observed upon hybridisation. The probe
CC   comprises a base sequence derived from a fully defined sequence of 1227
CC   nucleotides as given in the specification and being labelled at the 3' or
CC   5' end with a fluorescent dye. The probe of the invention may be useful
CC   for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC   beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC   detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC   contamination of the amplified product is prevented and the process is
CC   automated. The current sequence is that of the fluorescent-labelled probe
CC   (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC   receptor (B3AR) T190 variant DNA.
XX
SQ   Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 16; DB 13; Length 16;
 Best Local Similarity   100.0%; Pred. No. 1.3e+02;
 Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   1 CATCGCCTGGACTCCG 16
             ||||||||||||||||
o   1 CATCGCCTGGACTCCG 16

ESULT 2
AT58989
ID   AAT58989 standard; DNA; 17 BP.
XX
AC   AAT58989;
XX
DT   04-AUG-1997 (first entry)
XX
DE   Obesity and type II diabetes mellitus diagnosis nucleic acid probe.
XX
KW   Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;
KW   beta3AR; ss.
XX
OS   Synthetic.
XX
PN   WO9636641-A1.
XX
PD   21-NOV-1996.
XX
PF   17-MAY-1996;   96WO-US007218.
XX
PR   19-MAY-1995;   95US-00446530.

XX
PI Shuldiner AR, Walston J, Silver K, Roth J;
XX
PR WPI; 1997-012034/01.
XX
PT New isolated beta3-adrenergic receptor mutation - used to develop prods.
PT for the diagnosis and treatment of type II diabetes and/or obesity.
XX
PS Claim 17; Page 42; 51pp; English.
XX
CC The present sequence is a nucleic acid probe used in a method for
CC diagnosis of a subject having or at risk of having type II diabetes
CC mellitus and/or obesity. The method involves contacting a target nucleic
CC acid of a sample from the subject with a nucleic acid probe (preferably
CC the present sequence or that in AAT58990) that detects a mutation in the
CC beta3-adrenergic receptor (beta3AR) gene. The present sequence can also
CC be used in the treatment of subjects having or at risk of having type II
CC diabetes and/or obesity
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 16; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCG 16
              ||||||||||||||||
Db   1 CATCGCCTGGACTCCG 16

RESULT 3
AAT58987/c
ID AAT58987 standard; DNA; 17 BP.
XX
AC AAT58987;
XX
DT 04-AUG-1997 (first entry)
XX
DE Obesity and type II diabetes mellitus diagnosis target nucleic acid.
XX
KW Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;
KW beta3AR; ss.
XX
OS Synthetic.
XX
PN WO9636641-A1.
XX
PD 21-NOV-1996.
XX
PF 17-MAY-1996; 96WO-US007218.
XX
PR 19-MAY-1995; 95US-00446530.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI Shuldiner AR, Walston J, Silver K, Roth J;
XX
PR WPI; 1997-012034/01.
XX
PT New isolated beta3-adrenergic receptor mutation - used to develop prods.
PT for the diagnosis and treatment of type II diabetes and/or obesity.
XX
PS Claim 16; Page 42; 51pp; English.
XX
CC The present sequence is a target nucleic acid detected in a method for
CC diagnosis of a subject having or at risk of having type II diabetes
CC mellitus and/or obesity. The method involves contacting a target nucleic
CC acid of a sample from the subject (preferably the present sequence or
CC that in AAT58988) with a nucleic acid probe that detects a mutation in
CC the beta3-adrenergic receptor (beta3AR) gene

Q Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCG 16
   ||||||||||||||||
D 17 CATCGCCTGGACTCCG 2

ESULT 4
EC91758/c
D AEC91758 standard; DNA; 17 BP.
X
C AEC91758;
X
T 01-DEC-2005 (first entry)
X
E Probe 5T-B3AR-w-IMS-R2-17 SEQ ID NO:34.
X
W DNA detection; SNP detection; probe; ss.
X
S Synthetic.
X
N JP2005261354-A.
X
D 29-SEP-2005.
X
F 19-MAR-2004; 2004JP-00080974.
X
R 19-MAR-2004; 2004JP-00080974.
X
A (KYOT-) KYOTO DAIICHI KAGAKU KK.
X
I Inose K;
X
R WPI; 2005-662138/68.
X
T Detecting target nucleic acid, involves detecting target based on change
T of fluorescence intensity due to formation or dissociation of hybrid of
T target nucleic acid and hybridization probe having 5-carboxy fluorescein.
X
S Example 10; SEQ ID NO 34; 28pp; Japanese.
X
C The invention relates to a method (M1) for detecting a target nucleic
C acid. (M1) involves measuring the change of fluorescence intensity due to
C formation or dissociation of the hybrid of the hybridization probe
C comprising a labeled terminal portion, and a target nucleic acid, and
C detecting the target nucleic acid based on the change, where the
C hybridization probe is labeled using the fluorescent pigment chosen from
C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
C 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
C hydrazide (Cascade blue). Also described: (1) a real-time PCR method
C (M2), which involves carrying out real-time PCR using the hybridization
C probe labeled with the fluorescent pigment, where the hybridization probe
C is the probe labeled at its terminal with the fluorescent pigment chosen
C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
C curve analysis (M3), which involves using the hybridization probe labeled
C with the fluorescent pigment, where the hybridization probe is the probe
C labeled at its terminal with the fluorescent pigment chosen from TAMRA,
C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
C target nucleic acid and single nucleotide polymorphisms (SNPs), and in
C measurement of the ratio of normal type DNA and variant DNA. (M1) enables
C detection of the nucleic acid by fluorescent detection method, easily and
C cost effectively. The present sequence represents a probe used in an
C example from the present invention

Q Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCG 16
   ||||||||||||||||
D 17 CATCGCCTGGACTCCG 2

ESULT 5
DT93450
D ADT93450 standard; DNA; 18 BP.
K
C ADT93450;
K
I 13-JAN-2005 (first entry)
K
E Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.
K
W SNP detection; beta3 adrenaline receptor; ss; probe.
K
S Homo sapiens.
K
H Key Location/Qualifiers
F modified_base 1
F /*tag= a
F /mod_base= OTHER
F /note= "OTHER = Linked to BODIPY FL group"
F modified_base 18
F /*tag= b
F /mod_base= OTHER
F /note= "OTHER = Optionally linked to P group"
K
N WO2004092385-A1.
K
D 28-OCT-2004.
K
F 16-APR-2004; 2004WO-JP005525.
K
R 18-APR-2003; 2003JP-00114381.
K
A (ARKR-) ARKRAY INC.
K
I Hirai M;
K
R WPI; 2004-784610/77.
K
P Nucleic acid probe useful for detecting mutation in beta3 adrenaline
P receptor gene having single nucleotide polymorphism, labeled at terminal
P with fluorescent dye and shows decrease in fluorescence of fluorescent
P dye upon hybridization.
K
S Claim 2; SEQ ID NO 10; 31pp; Japanese.
K
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the fluorescent-labelled probe
C (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
C receptor (B3AR) T190 variant DNA.

Sequence 16 BP; 3 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCCG 16
             ||||||||||||||||
D          1 CATCGCCTGGACTCCG 16
```

ESULT 6
3K50102
D ABK50102 standard; DNA; 19 BP.
K
C ABK50102;
K
R 15-JUL-2002 (first entry)
K
E Allele specific hybridisation probe.
K
W Optimal reagent oligonucleotide; target nucleic acid evaluation;
W target feature; exclusion value; ranking value; sequence window;
W hybridisation; probe; ss.
K
S Synthetic.
K
N WO200229379-A2.
K
D 11-APR-2002.
K
F 04-OCT-2001; 2001WO-US031037.
K
R 04-OCT-2000; 2000US-0237383P.
K
A (CELA-) CELADON LAB INC.
K
I Peterson RJ;
K
R WPI; 2002-340129/37.
K
T Determining an optimal reagent oligonucleotide for evaluating a target
T nucleic acid having a target feature, involves defining a set of
T exclusion values and/or ranking values specific to a biochemical method.
K
S Example; Fig 2A; 91pp; English.
K
C The present invention relates to a new method for determining an optimal
C reagent oligonucleotide for evaluating a target nucleic acid having a
C target feature. The method comprises defining a set of exclusion values
C and/or ranking values specific to the method, defining a sequence window
C adjacent to the target, and generating candidate reagent oligonucleotides
C complementary to the sense and/or antisense strands of the target within
C the window. The method can be used for determining an optimal reagent
C oligonucleotide sequence for use in a biochemical method for evaluating a
C target nucleic acid sequence having a target feature. The present nucleic
C acid sequence represent an allele specific hybridisation probe that was
C used in the methods of the invention in numbering systems
K
Q Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCCG 16
             ||||||||||||||||
D          3 CATCGCCTGGACTCCG 18
```

ESULT 7

ID   ADT93449 standard; DNA; 20 BP.
XX
AC   ADT93449;
XX
DT   13-JAN-2005 (first entry)
XX
DE   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.
XX
KW   SNP detection; beta3 adrenaline receptor; ss; probe.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   modified_base   1
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "OTHER = Linked to BODIPY FL group"
FT   modified_base   20
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "OTHER = Linked to P group"
XX
PN   WO2004092385-A1.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-JP005525.
XX
PR   18-APR-2003; 2003JP-00114381.
XX
PA   (ARKR-) ARKRAY INC.
XX
PI   Hirai M;
XX
DR   WPI; 2004-784610/77.
XX
PT   Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT   receptor gene having single nucleotide polymorphism, labeled at terminal
PT   with fluorescent dye and shows decrease in fluorescence of fluorescent
PT   dye upon hybridization.
XX
PS   Claim 2; SEQ ID NO 9; 31pp; Japanese.
XX
CC   The invention relates to a novel nucleic acid probe which is labelled at
CC   a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC   of the fluorescent dye is observed upon hybridisation. The probe
CC   comprises a base sequence derived from a fully defined sequence of 1227
CC   nucleotides as given in the specification and being labelled at the 3' or
CC   5' end with a fluorescent dye. The probe of the invention may be useful
CC   for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC   beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC   detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC   contamination of the amplified product is prevented and the process is
CC   automated. The current sequence is that of the fluorescent-labelled probe
CC   (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC   receptor (B3AR) T190 variant DNA.
XX
SQ   Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 16; DB 13; Length 20;
 Best Local Similarity   100.0%; Pred. No. 1.3e+02;
 Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCG 16
              ||||||||||||||||
Db   1 CATCGCCTGGACTCCG 16

RESULT 8
AF96885

XX
AC   AAF96885;
XX
DT   18-NOV-2004 (revised)
DT   06-JUN-2001 (first entry)
XX
DE   Human gene single nucleotide polymorphism #1646.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   variation   11
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 159; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
CC
CC   Revised record issued on 18-NOV-2004 : The variantion feature was
CC   incorrectly given a captial V
XX
SQ   Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 16; DB 4; Length 21;
 Best Local Similarity   100.0%; Pred. No. 1.3e+02;
 Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   1 CATCGCCTGGACTCCG 16
             ||||||||||||||||
D   4 CATCGCCTGGACTCCG 19

ESULT 9
DO26525
D ADO26525 standard; DNA; 25 BP.
K
C ADO26525;
K
I 12-AUG-2004 (first entry)
K
E Novel hybridisation detection-related oligonucleotide SeqID1.
K
W hybridisation detection; immobilised probe; AC impedance;
W foetal genome analysis; ss.
K
S Unidentified.
K
N WO2004044570-A1.
K
D 27-MAY-2004.
K
F 30-SEP-2003; 2003WO-JP012499.
K
R 14-NOV-2002; 2002JP-00331059.
K
A (TOYA-) TOYAMA PREFECTURE.
A (COSE-) COSEL CO LTD.
A (TATE-) TATEYAMA KAGAKU IND CO LTD.
A (TOXX) TOYO KAKO CO LTD.
K
I Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
I Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
K
R WPI; 2004-420427/39.
K
T Detection of hybridization of an immobilized probe to a target nucleic
T acid by measuring AC impedance across the carrier surface for specific
T gene detection in investigation and diagnosis of disease.
K
S Example; SEQ ID NO 1; 33pp; Japanese.
K
C This invention relates to a novel method of detecting hybridisation of an
C immobilised probe to a target nucleic acid using measurement of AC
C impedance. Detection of specific genes and gene sequences in nucleic acid
C samples (such as samples of genomic DNA) may be useful for diagnosis,
C prediction and prevention of genetic disorders and analysis of foetal
C genome. Hybridisation is detected with high accuracy and sensitivity
C without the use of dyes. The present sequence is that of an
C oligonucleotide which was used in the exemplification of the invention.
K
Q Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

 Query Match   100.0%; Score 16; DB 12; Length 25;
 Best Local Similarity   100.0%; Pred. No. 1.3e+02;
 Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   1 CATCGCCTGGACTCCG 16
             ||||||||||||||||
D   6 CATCGCCTGGACTCCG 21

ESULT 10
BL40567
D ABL40567 standard; DNA; 26 BP.
K
C ABL40567;
K
I 17-JUN-2002 (first entry)
K
E Primer #7 used in a base polymorphism detection method.
K
W Polymorphism; nucleic acid detection; endonuclease; probe; ADBB2;

XX
SY   Synthetic.
XX
PN   JP2002034598-A.
XX
PD   05-FEB-2002.
XX
PF   27-JUL-2000; 2000JP-00226912.
XX
PR   27-JUL-2000; 2000JP-00226912.
XX
PA   (TOYM) TOYOBO KK.
XX
DR   WPI; 2002-298820/34.
XX
PT   Detection of base polymorphism.
XX
PS   Disclosure; Page 10; 10pp; Japanese.
XX
CC   The invention relates to a method for detecting base polymorphism. The
CC   method involves (1) amplifying the nucleic acid fragment containing base
CC   polymorphism of the specific nucleic acid sequence; (2) hybridising the
CC   amplified nucleic acid with at least two polymorphism-specific probes;
CC   (3) treating with RNA-selective cleavage endonuclease; (4) measuring
CC   detecting signals of each probe; and (5) identifying polymorphism by the
CC   ratio of each detecting signals. The probe can be used for detecting base
CC   polymorphism. The present sequence represents a PCR primer used in the
CC   course of the invention
XX
SQ   Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

 Query Match   100.0%; Score 16; DB 6; Length 26;
 Best Local Similarity   100.0%; Pred. No. 1.3e+02;
 Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCG 16
              ||||||||||||||||
Db   9 CATCGCCTGGACTCCG 24

RESULT 11
ADT93453
ID   ADT93453 standard; DNA; 34 BP.
XX
AC   ADT93453;
XX
DT   13-JAN-2005 (first entry)
XX
DE   Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.
XX
KW   single nucleotide polymorphism; SNP; SNP detection;
KW   beta3 adrenaline receptor; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   replace(19,C)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO2004092385-A1.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-JP005525.
XX
PR   18-APR-2003; 2003JP-00114381.
XX
PA   (ARKR-) ARKRAY INC.

XX

RN WPI; 2004-784610/77.

XX

PT Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT receptor gene having single nucleotide polymorphism, labeled at terminal
PT with fluorescent dye and shows decrease in fluorescence of fluorescent
PT dye upon hybridization.

XX

PS Example 1; Fig 1; 31pp; Japanese.

XX

CC The invention relates to a novel nucleic acid probe which is labelled at
CC a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC of the fluorescent dye is observed upon hybridisation. The probe
CC comprises a base sequence derived from a fully defined sequence of 1227
CC nucleotides as given in the specification and being labelled at the 3' or
CC 5' end with a fluorescent dye. The probe of the invention may be useful
CC for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC contamination of the amplified product is prevented and the process is
CC automated. The current sequence is that of the human beta3 adrenaline
CC receptor (B3AR) T190 variant DNA fragment of the invention.

XX

SQ Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCG 16
||||||||||||||||
D 12 CATCGCCTGGACTCCG 27

ESULT 12
AC73164
ID AAC73164 standard; DNA; 21 BP.
XX
AC AAC73164;
XX
DT 02-FEB-2001 (first entry)
XX
DE SNP flanking sequence #24 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.

Example 7; Page 50; 70pp; English.

The present invention relates to an oligonucleotide array comprising oligonucleotide tags fixed to a solid substrate. The oligonucleotide array is useful for genotyping a nucleic acid sample at one or more loci via single base extension (SBE) reactions. A pair of primers is used to amplify a polymorphic locus in a sample e.g. a single nucleotide polymorphism (SNP). The present sequence is one such polymorphic locus used in the present invention. The amplified nucleic acid product is then used as a template in a SBE reaction with an extension primer. The SBE reaction products are used to form the oligonucleotide array. Note: This sequence includes a SNP represented by the degenerate codon in the sequence

Sequence 21 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 1 Other;

Query Match 100.0%; Score 16; DB 3; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCCG 16
             ||||||:||||||||
D          4 CATCGCCYGGACTCCG 19
```

ESULT 13
AA04696
AAA04696 standard; DNA; 29 BP.

AAA04696;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene ADRB3.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.
03-MAY-1999; 99US-00304232.

(AFFY-) AFFYMETRIX INC.
(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Disclosure; Page 45; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be

used for association studies for hypertension, and in hypertension
diagnostic assays. Where the polymorphisms have strong correlation with
hypertension, within a gene, they are likely to have a causative role in
hypertension. This information can be used to find the precise role of a
polymorphism in the disease, and this can be used to identify potential
drugs which combat the disease. The polymorphisms can be tested for
association with other diseases e.g. agammaglobulinemia, diabetes
insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
syndrome, Fabrys disease, familial hypercholesterolemia, polycystic
kidney disease, hereditary spherocytosis, von Willebrands disease,
tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
acute intermittent porphyria. The polymorphic forms can also be used in
forensics to identify individuals

Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 16; DB 3; Length 29;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCCG 16
             ||||||:||||||||
o          8 CATCGCCYGGACTCCG 23
```

ESULT 14
3K50101
ABK50101 standard; DNA; 41 BP.

ABK50101;

15-JUL-2002 (first entry)

Nucleic acid sequence used for sequence formatting.

Optimal reagent oligonucleotide; target nucleic acid evaluation;
target feature; exclusion value; ranking value; sequence window;
sequence formatting; ds.

Synthetic.

WO200229379-A2.

11-APR-2002.

04-OCT-2001; 2001WO-US031037.

04-OCT-2000; 2000US-0237383P.

(CELA-) CELADON LAB INC.

Peterson RJ;

WPI; 2002-340129/37.

Determining an optimal reagent oligonucleotide for evaluating a target
nucleic acid having a target feature, involves defining a set of
exclusion values and/or ranking values specific to a biochemical method.

Example; Fig 1B; 91pp; English.

The present invention relates to a new method for determining an optimal
reagent oligonucleotide for evaluating a target nucleic acid having a
target feature. The method comprises defining a set of exclusion values
and/or ranking values specific to the method, defining a sequence window
adjacent to the target, and generating candidate reagent oligonucleotides
complementary to the sense and/or antisense strands of the target within
the window. The method can be used for determining an optimal reagent
oligonucleotide sequence for use in a biochemical method for evaluating a
target nucleic acid sequence having a target feature. The present nucleic

C invention for nucleic acid sequence formatting
K
Q Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

Query Match 100.0%; Score 16; DB 6; Length 41;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCG 16
     ||||||:||||||||
D 14 CATCGCCYGGACTCCG 29

ESULT 15
DT93452
D ADT93452 standard; DNA; 15 BP.
K
C ADT93452;
K
I 13-JAN-2005 (first entry)

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104100_us-10-553-509-12.szlm60.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104100_us-10-53-509-12.szlm60.rng.

tart | next page

Go Back to previous pag

```
                        GenCore version 5.1.9
                  Copyright (c) 1993 - 2006  Biocceleration Ltd.


M nucleic - nucleic search, using sw model

un on:          December 15, 2006, 05:57:43 ; Search time 180.843 Seconds
                                          (without alignments)
                                          578.313 Million cell updates/sec

itle:           US-10-553-509-12
erfect score:   15
equence:        1 catcgcctggactcc 15

coring table:   IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

earched:        5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters:      5397982

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase :        N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

                 %
esult            Query
  No.    Score  Match Length DB  ID                          Description
---------------------------------------------------------------------------
```

	3	15	100.0	17	2	AAT58989	Aat58989 Obesity a
	4	15	100.0	17	2	AAT58987	Aat58987 Obesity a
	5	15	100.0	17	14	AEC91758	Aec91758 Probe 5T-
	6	15	100.0	18	13	ADT93450	Adt93450 Fluoresce
	7	15	100.0	19	6	ABK50102	Abk50102 Allele sp
	8	15	100.0	20	13	ADT93449	Adt93449 Fluoresce
	9	15	100.0	21	4	AAF96885	Aaf96885 Human gen
	10	15	100.0	25	12	ADO26525	Ado26525 Novel hyb
	11	15	100.0	26	6	ABL40567	Abl40567 Primer #7
	12	15	100.0	34	13	ADT93453	Adt93453 Human bet
	13	14.6	100.0	21	3	AAC73164	Aac73164 SNP flank
	14	14.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
	15	14.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
	16	14	93.3	18	14	AEC91756	Aec91756 Probe 3T-
	17	14	93.3	51	4	AAH90342	Aah90342 Human clo
	18	14	93.3	51	4	AAH90341	Aah90341 Human clo
	19	13.4	89.3	16	13	ADT93445	Adt93445 Fluoresce
	20	13.4	89.3	17	2	AAT58988	Aat58988 Obesity a
	21	13.4	89.3	17	2	AAT58990	Aat58990 Obesity a
	22	13.4	89.3	19	13	ADT93446	Adt93446 Fluoresce
	23	13.4	89.3	21	14	AEC91760	Aec91760 Probe 3T-
	24	13.4	89.3	25	4	AAC89164	Aac89164 Sample DN
	25	13.4	89.3	25	6	ABL40568	Abl40568 Primer #8
	26	13.4	89.3	25	12	ADO26526	Ado26526 Novel hyb
	27	13.4	89.3	33	2	AAQ87254	Aaq87254 Primer fo
	28	13.4	89.3	34	13	ADT93454	Adt93454 Human bet
	29	13.4	89.3	35	2	AAV24264	Aav24264 Chimeric
	30	13.4	89.3	35	2	AAX00108	Aax00108 Human ant
	31	13.4	89.3	35	3	AAZ58889	Aaz58889 PCR prime
	32	13.4	89.3	35	4	AAF69217	Aaf69217 Chimeric
	33	13.4	89.3	35	4	AAF69105	Aaf69105 Chimeric
	34	13.4	89.3	35	4	AAH75082	Aah75082 Nucleotid
	35	13.4	89.3	35	4	AAH76620	Aah76620 Chimeric
	36	13.4	89.3	35	5	AAH74261	Aah74261 Nucleotid
	37	13.4	89.3	35	5	AAF69161	Aaf69161 Chimeric
	38	13.4	89.3	35	6	ABL94797	Abl94797 Joint dis
	39	13.4	89.3	35	10	ABT31649	Abt31649 Angiogene
	40	13.4	89.3	35	12	ADO33818	Ado33818 Parathyro
	41	13.4	89.3	39	2	AAQ35923	Aaq35923 Human/mon
	42	13.4	89.3	39	2	AAT92223	Aat92223 Monkey/hu
	43	13.4	89.3	39	2	AAT62895	Aat62895 Human or
	44	13.4	89.3	39	2	AAT95148	Aat95148 Human or
	45	13.4	89.3	39	2	AAV05670	Aav05670 Human/mon

ALIGNMENTS

```
ESULT 1
DT93452
D   ADT93452 standard; DNA; 15 BP.
K
C   ADT93452;
K
R   13-JAN-2005  (first entry)
K
E   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 12.
K
W   SNP detection; beta3 adrenaline receptor; ss; probe.
K
S   Homo sapiens.
K
H   Key             Location/Qualifiers
F   modified_base   1
F                   /*tag=  a
F                   /mod_base= OTHER
F                   /note= "OTHER = Linked to BODIPY FL group"
F   modified_base   15
F                   /*tag=  b
F                   /mod_base= OTHER
```

XX
PN   WO2004092385-A1.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-JP005525.
XX
PR   18-APR-2003; 2003JP-00114381.
XX
PA   (ARKR-) ARKRAY INC.
XX
PI   Hirai M;
XX
DR   WPI; 2004-784610/77.
XX
PT   Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT   receptor gene having single nucleotide polymorphism, labeled at terminal
PT   with fluorescent dye and shows decrease in fluorescence of fluorescent
PT   dye upon hybridization.
XX
PS   Claim 2; SEQ ID NO 12; 31pp; Japanese.
XX
CC   The invention relates to a novel nucleic acid probe which is labelled at
CC   a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC   of the fluorescent dye is observed upon hybridisation. The probe
CC   comprises a base sequence derived from a fully defined sequence of 1227
CC   nucleotides as given in the specification and being labelled at the 3' or
CC   5' end with a fluorescent dye. The probe of the invention may be useful
CC   for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC   beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC   detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC   contamination of the amplified product is prevented and the process is
CC   automated. The current sequence is that of the fluorescent-labelled probe
CC   (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC   receptor (B3AR) T190 variant DNA.
XX
SQ   Sequence 15 BP; 2 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 15; DB 13; Length 15;
 Best Local Similarity   100.0%; Pred. No. 2.3e+02;
 Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCC 15
              |||||||||||||||
Db   1 CATCGCCTGGACTCC 15

RESULT 2
ADT93451
ID   ADT93451 standard; DNA; 16 BP.
XX
AC   ADT93451;
XX
DT   13-JAN-2005 (first entry)
XX
DE   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 11.
XX
KW   SNP detection; beta3 adrenaline receptor; ss; probe.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   modified_base   1
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "OTHER = Linked to BODIPY FL group"
FT   modified_base   16
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "OTHER = Optionally linked to R group"

N WO2004092385-A1.
X
D 28-OCT-2004.
X
F 16-APR-2004; 2004WO-JP005525.
X
R 18-APR-2003; 2003JP-00114381.
X
A (ARKR-) ARKRAY INC.
X
I Hirai M;
X
R WPI; 2004-784610/77.
X
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline
T receptor gene having single nucleotide polymorphism, labeled at terminal
T with fluorescent dye and shows decrease in fluorescence of fluorescent
T dye upon hybridization.
X
S Claim 2; SEQ ID NO 11; 31pp; Japanese.
X
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the fluorescent-labelled probe
C (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
C receptor (B3AR) T190 variant DNA.
X
S Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y . 1 CATCGCCTGGACTCC 15
||||||||||||||
o 1 CATCGCCTGGACTCC 15

ESULT 3
AT58989
D AAT58989 standard; DNA; 17 BP.
X
C AAT58989;
X
I 04-AUG-1997 (first entry)
X
E Obesity and type II diabetes mellitus diagnosis nucleic acid probe.
X
K Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;
K beta3AR; ss.
X
S Synthetic.
X
N WO9636641-A1.
X
D 21-NOV-1996.
X
F 17-MAY-1996; 96WO-US007218.
X
R 19-MAY-1995; 95US-00446530.
X
A (UYJO) UNIV JOHNS HOPKINS SCHOOL MED

I Shuldiner AR, Walston J, Silver K, Roth J;
X
R WPI; 1997-012034/01.
X
T New isolated beta3-adrenergic receptor mutation - used to develop prods.
T for the diagnosis and treatment of type II diabetes and/or obesity.
X
S Claim 17; Page 42; 51pp; English.
X
C The present sequence is a nucleic acid probe used in a method for
C diagnosis of a subject having or at risk of having type II diabetes
C mellitus and/or obesity. The method involves contacting a target nucleic
C acid of a sample from the subject with a nucleic acid probe (preferably
C the present sequence or that in AAT58990) that detects a mutation in the
C beta3-adrenergic receptor (beta3AR) gene. The present sequence can also
C be used in the treatment of subjects having or at risk of having type II
C diabetes and/or obesity
X
Q Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 15; DB 2; Length 17;
 Best Local Similarity   100.0%; Pred. No. 2.3e+02;
 Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   1 CATCGCCTGGACTCC 15
           ||||||||||||||||
D   1 CATCGCCTGGACTCC 15

ESULT 4
AT58987/c
D AAT58987 standard; DNA; 17 BP.
X
C AAT58987;
X
T 04-AUG-1997 (first entry)
X
E Obesity and type II diabetes mellitus diagnosis target nucleic acid.
X
W Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;
W beta3AR; ss.
X
S Synthetic.
X
N WO9636641-A1.
X
D 21-NOV-1996.
X
F 17-MAY-1996;   96WO-US007218.
X
R 19-MAY-1995;   95US-00446530.
X
A (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
X
I Shuldiner AR, Walston J, Silver K, Roth J;
X
R WPI; 1997-012034/01.
X
T New isolated beta3-adrenergic receptor mutation - used to develop prods.
T for the diagnosis and treatment of type II diabetes and/or obesity.
X
S Claim 16; Page 42; 51pp; English.
X
C The present sequence is a target nucleic acid detected in a method for
C diagnosis of a subject having or at risk of having type II diabetes
C mellitus and/or obesity. The method involves contacting a target nucleic
C acid of a sample from the subject (preferably the present sequence or
C that in AAT58988) with a nucleic acid probe that detects a mutation in
C the beta3-adrenergic receptor (beta3AR) gene
V

Query Match 100.0%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15
||||||||||||||||
C 17 CATCGCCTGGACTCC 3

ESULT 5
EC91758/c
D AEC91758 standard; DNA; 17 BP.
K
C AEC91758;
K
T 01-DEC-2005 (first entry)
K
E Probe 5T-B3AR-w-IMS-R2-17 SEQ ID NO:34.
K
W DNA detection; SNP detection; probe; ss.
K
S Synthetic.
K
N JP2005261354-A.
K
D 29-SEP-2005.
K
F 19-MAR-2004; 2004JP-00080974.
K
R 19-MAR-2004; 2004JP-00080974.
K
A (KYOT-) KYOTO DAIICHI KAGAKU KK.
K
I Inose K;
K
R WPI; 2005-662138/68.
K
T Detecting target nucleic acid, involves detecting target based on change
T of fluorescence intensity due to formation or dissociation of hybrid of
T target nucleic acid and hybridization probe having 5-carboxy fluorescein.
K
S Example 10; SEQ ID NO 34; 28pp; Japanese.
K
C The invention relates to a method (M1) for detecting a target nucleic
C acid. (M1) involves measuring the change of fluorescence intensity due to
C formation or dissociation of the hybrid of the hybridization probe
C comprising a labeled terminal portion, and a target nucleic acid, and
C detecting the target nucleic acid based on the change, where the
C hybridization probe is labeled using the fluorescent pigment chosen from
C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
C 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
C hydrazide (Cascade blue). Also described: (1) a real-time PCR method
C (M2), which involves carrying out real-time PCR using the hybridization
C probe labeled with the fluorescent pigment, where the hybridization probe
C is the probe labeled at its terminal with the fluorescent pigment chosen
C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
C curve analysis (M3), which involves using the hybridization probe labeled
C with the fluorescent pigment, where the hybridization probe is the probe
C labeled at its terminal with the fluorescent pigment chosen from TAMRA,
C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
C target nucleic acid and single nucleotide polymorphisms (SNPs), and in
C measurement of the ratio of normal type DNA and variant DNA. (M1) enables
C detection of the nucleic acid by fluorescent detection method, easily and
C cost effectively. The present sequence represents a probe used in an
C example from the present invention.

Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15
||||||||||||||||
D 17 CATCGCCTGGACTCC 3

ESULT 6
DT93450
D ADT93450 standard; DNA; 18 BP.
K
C ADT93450;
K
R 13-JAN-2005 (first entry)
K
E Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.
K
W SNP detection; beta3 adrenaline receptor; ss; probe.
K
S Homo sapiens.
K
H Key Location/Qualifiers
F modified_base 1
F /*tag= a
F /mod_base= OTHER
F /note= "OTHER = Linked to BODIPY FL group"
F modified_base 18
F /*tag= b
F /mod_base= OTHER
F /note= "OTHER = Optionally linked to P group"
K
N WO2004092385-A1.
K
D 28-OCT-2004.
K
F 16-APR-2004; 2004WO-JP005525.
K
R 18-APR-2003; 2003JP-00114381.
K
A (ARKR-) ARKRAY INC.
K
I Hirai M;
K
R WPI; 2004-784610/77.
K
P Nucleic acid probe useful for detecting mutation in beta3 adrenaline
P receptor gene having single nucleotide polymorphism, labeled at terminal
P with fluorescent dye and shows decrease in fluorescence of fluorescent
P dye upon hybridization.
K
S Claim 2; SEQ ID NO 10; 31pp; Japanese.
K
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the fluorescent-labelled probe
C (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
C receptor (B3AR) T190 variant DNA.
K

```
 Query Match             100.0%;  Score 15;  DB 13;  Length 18;
 Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
 Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Y          1 CATCGCCTGGACTCC 15
             |||||||||||||||
D          1 CATCGCCTGGACTCC 15


ESULT 7
3K50102
D   ABK50102 standard; DNA; 19 BP.
K
C   ABK50102;
K
F   15-JUL-2002  (first entry)
K
E   Allele specific hybridisation probe.
K
W   Optimal reagent oligonucleotide; target nucleic acid evaluation;
W   target feature; exclusion value; ranking value; sequence window;
W   hybridisation; probe; ss.
K
S   Synthetic.
K
N   WO200229379-A2.
K
D   11-APR-2002.
K
F   04-OCT-2001; 2001WO-US031037.
K
R   04-OCT-2000; 2000US-0237383P.
K
A   (CELA-) CELADON LAB INC.
K
I   Peterson RJ;
K
R   WPI; 2002-340129/37.
K
P   Determining an optimal reagent oligonucleotide for evaluating a target
P   nucleic acid having a target feature, involves defining a set of
P   exclusion values and/or ranking values specific to a biochemical method.
K
S   Example; Fig 2A; 91pp; English.
K
C   The present invention relates to a new method for determining an optimal
C   reagent oligonucleotide for evaluating a target nucleic acid having a
C   target feature. The method comprises defining a set of exclusion values
C   and/or ranking values specific to the method, defining a sequence window
C   adjacent to the target, and generating candidate reagent oligonucleotides
C   complementary to the sense and/or antisense strands of the target within
C   the window. The method can be used for determining an optimal reagent
C   oligonucleotide sequence for use in a biochemical method for evaluating a
C   target nucleic acid sequence having a target feature. The present nucleic
C   acid sequence represent an allele specific hybridisation probe that was
C   used in the methods of the invention in numbering systems
K
Q   Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

 Query Match             100.0%;  Score 15;  DB 6;  Length 19;
 Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
 Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Y          1 CATCGCCTGGACTCC 15
             |||||||||||||||
D          3 CATCGCCTGGACTCC 17


ESULT 8
```

XX

AC ADT93449;

XX

DT 13-JAN-2005 (first entry)

XX

DE Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.

XX

KW SNP detection; beta3 adrenaline receptor; ss; probe.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER = Linked to BODIPY FL group"

FT modified_base 20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "OTHER = Linked to P group"

XX

PN WO2004092385-A1.

XX

PD 28-OCT-2004.

XX

PF 16-APR-2004; 2004WO-JP005525.

XX

PR 18-APR-2003; 2003JP-00114381.

XX

PA (ARKR-) ARKRAY INC.

XX

PI Hirai M;

XX

DR WPI; 2004-784610/77.

XX

PT Nucleic acid probe useful for detecting mutation in beta3 adrenaline

PT receptor gene having single nucleotide polymorphism, labeled at terminal

PT with fluorescent dye and shows decrease in fluorescence of fluorescent

PT dye upon hybridization.

XX

PS Claim 2; SEQ ID NO 9; 31pp; Japanese.

XX

CC The invention relates to a novel nucleic acid probe which is labelled at
CC a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC of the fluorescent dye is observed upon hybridisation. The probe
CC comprises a base sequence derived from a fully defined sequence of 1227
CC nucleotides as given in the specification and being labelled at the 3' or
CC 5' end with a fluorescent dye. The probe of the invention may be useful
CC for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC contamination of the amplified product is prevented and the process is
CC automated. The current sequence is that of the fluorescent-labelled probe
CC (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC receptor (B3AR) T190 variant DNA.

XX

SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCC 15
||||||||||||||||
Db 1 CATCGCCTGGACTCC 15

RESULT 9
AAF96885

AAF96885;

18-NOV-2004 (revised)
06-JUN-2001 (first entry)

Human gene single nucleotide polymorphism #1646.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

Homo sapiens.
Unidentified.

Key	Location/Qualifiers
variation	11
	/*tag= a
	/standard_name= "Single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.
26-JUL-2000; 2000US-0220947P.
16-AUG-2000; 2000US-0225724P.

(WHED) WHITEHEAD INST BIOMEDICAL RES.
(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;

WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.

Example; Page 159; 242pp; English.

The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification

Revised record issued on 18-NOV-2004 : The variantion feature was incorrectly given a captial V

Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCC 15
             |||||||||||||||
D          4 CATCGCCTGGACTCC 18
```

DO26525
D ADO26525 standard; DNA; 25 BP.
X
C ADO26525;
X
R 12-AUG-2004 (first entry)
X
E Novel hybridisation detection-related oligonucleotide SeqID1.
X
W hybridisation detection; immobilised probe; AC impedance;
W foetal genome analysis; ss.
X
S Unidentified.
X
N WO2004044570-A1.
X
D 27-MAY-2004.
X
F 30-SEP-2003; 2003WO-JP012499.
X
R 14-NOV-2002; 2002JP-00331059.
X
A (TOYA-) TOYAMA PREFECTURE.
A (COSE-) COSEL CO LTD.
A (TATE-) TATEYAMA KAGAKU IND CO LTD.
A (TOXX) TOYO KAKO CO LTD.
X
I Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
I Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
X
R WPI; 2004-420427/39.
X
P Detection of hybridization of an immobilized probe to a target nucleic
P acid by measuring AC impedance across the carrier surface for specific
P gene detection in investigation and diagnosis of disease.
X
S Example; SEQ ID NO 1; 33pp; Japanese.
X
C This invention relates to a novel method of detecting hybridisation of an
C immobilised probe to a target nucleic acid using measurement of AC
C impedance. Detection of specific genes and gene sequences in nucleic acid
C samples (such as samples of genomic DNA) may be useful for diagnosis,
C prediction and prevention of genetic disorders and analysis of foetal
C genome. Hybridisation is detected with high accuracy and sensitivity
C without the use of dyes. The present sequence is that of an
C oligonucleotide which was used in the exemplification of the invention.
X
S Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match   100.0%; Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   1 CATCGCCTGGACTCC 15
             |||||||||||||||
D   6 CATCGCCTGGACTCC 20

ESULT 11
BL40567
D ABL40567 standard; DNA; 26 BP.
X
C ABL40567;
X
R 17-JUN-2002 (first entry)
X
E Primer #7 used in a base polymorphism detection method.
X
W Polymorphism; nucleic acid detection; endonuclease; probe; ADRB2;
W hybridisation; PCR primer; ss.

SS Synthetic.
XX
RN JP2002034598-A.
XX
RD 05-FEB-2002.
XX
PF 27-JUL-2000; 2000JP-00226912.
XX
PR 27-JUL-2000; 2000JP-00226912.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 2002-298820/34.
XX
PT Detection of base polymorphism.
XX
PS Disclosure; Page 10; 10pp; Japanese.
XX
CC The invention relates to a method for detecting base polymorphism. The
CC method involves (1) amplifying the nucleic acid fragment containing base
CC polymorphism of the specific nucleic acid sequence; (2) hybridising the
CC amplified nucleic acid with at least two polymorphism-specific probes;
CC (3) treating with RNA-selective cleavage endonuclease; (4) measuring
CC detecting signals of each probe; and (5) identifying polymorphism by the
CC ratio of each detecting signals. The probe can be used for detecting base
CC polymorphism. The present sequence represents a PCR primer used in the
CC course of the invention
XX
SQ Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

 Query Match   100.0%; Score 15; DB 6; Length 26;
 Best Local Similarity   100.0%; Pred. No. 2.3e+02;
 Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCC 15
              ||||||||||||||
Db   9 CATCGCCTGGACTCC 23

RESULT 12
ADT93453
ID ADT93453 standard; DNA; 34 BP.
XX
AC ADT93453;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.
XX
KW single nucleotide polymorphism; SNP; SNP detection;
KW beta3 adrenaline receptor; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT variation   replace(19,C)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
RN WO2004092385-A1.
XX
RD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-JP005525.
XX
PR 18-APR-2003; 2003JP-00114381.
XX
PA (ARKR-) ARKRAY INC.
XX
PI Hirai M.

R WPI; 2004-784610/77.
K
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline
T receptor gene having single nucleotide polymorphism, labeled at terminal
T with fluorescent dye and shows decrease in fluorescence of fluorescent
T dye upon hybridization.
K
S Example 1; Fig 1; 31pp; Japanese.
K
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the human beta3 adrenaline
C receptor (B3AR) T190 variant DNA fragment of the invention.
K
Q Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15
||||||||||||||||
D 12 CATCGCCTGGACTCC 26

ESULT 13
AC73164
D AAC73164 standard; DNA; 21 BP.
K
C AAC73164;
K
T 02-FEB-2001 (first entry)
K
E SNP flanking sequence #24 used in multiplexing PCR/SBE assay.
K
W Oligonucleotide array; genotyping; single base extension reaction; SBE;
W polymorphic locus; single nucleotide polymorphism; ss.
K
S Unidentified.
K
N WO200058516-A2.
K
D 05-OCT-2000.
K
F 27-MAR-2000; 2000WO-US008069.
K
R 26-MAR-1999; 99US-0126473P.
R 23-JUN-1999; 99US-0140359P.
K
A (WHED) WHITEHEAD INST BIOMEDICAL RES.
A (AFFY-) AFFYMETRIX INC.
K
I Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
I Ryder T, Sklar P;
K
R WPI; 2000-656171/63.
K
T Universal array of oligonucleotides tags attached to a solid substrate
T along with locus-specific tagged oligonucleotides useful in genotyping
T using single base extension reactions.
K
E Example 7; Page 50; 70pp; English

CC   The present invention relates to an oligonucleotide array comprising
CC   oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC   array is useful for genotyping a nucleic acid sample at one or more loci
CC   via single base extension (SBE) reactions. A pair of primers is used to
CC   amplify a polymorphic locus in a sample e.g. a single nucleotide
CC   polymorphism (SNP). The present sequence is one such polymorphic locus
CC   used in the present invention. The amplified nucleic acid product is then
CC   used as a template in a SBE reaction with an extension primer. The SBE
CC   reaction products are used to form the oligonucleotide array. Note: This
CC   sequence includes a SNP represented by the degenerate codon in the
CC   sequence
XX
SQ   Sequence 21 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 1 Other;

 Query Match   100.0%; Score 15; DB 3; Length 21;
 Best Local Similarity   93.3%; Pred. No. 3.8e+02;
 Matches   14; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCC 15
              ||||||:|||||||
Db   4 CATCGCCYGGACTCC 18

RESULT 14
AAA04696
ID   AAA04696 standard; DNA; 29 BP.
XX
AC   AAA04696;
XX
DT   22-MAY-2000 (first entry)
XX
DE   Polymorphic fragment of hypertension associated gene ADRB3.
XX
KW   Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW   Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW   Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
KW   polycystic kidney disease; von Willebrands disease; forensic; human;
KW   tuberous sclerosis; hereditary hemorrhagica telangiectasia;
KW   familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW   Ehlers-Danlos syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   EP955382-A2.
XX
PD   10-NOV-1999.
XX
PF   07-MAY-1999;   99EP-00250150.
XX
PR   07-MAY-1998;   98US-0084641P.
PR   03-MAY-1999;   99US-00304232.
XX
PA   (AFFY-) AFFYMETRIX INC.
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   Fan JB, Chakravarti A, Haluska MK;
XX
DR   WPI; 2000-107928/10.
XX
PT   Novel nucleic acids containing polymorphisms used in the diagnosis of
PT   hypertension.
XX
OS   Disclosure; Page 45; 53pp; English.
XX
CC   The invention provides polymorphic fragments of genes associated with
CC   hypertension. The nucleic acids including the polymorphic sites can be
CC   used as probes or primers for expressing variant proteins. Detection of
CC   the polymorphisms is useful in designing prophylactic and therapeutic
CC   regimes customized to underlying abnormalities. The polymorphisms can be
CC   used for association studies for hypertension, and in hypertension

hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 15; DB 3; Length 29;
Best Local Similarity 93.3%; Pred. No. 3.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCC 15

tart | next page

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104105_us-10-553-509-11.szlm60.rni.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104105_us-10-53-509-11.szlm60.rni.

tart

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 06:40:47 ; Search time 57.7079 Seconds
(without alignments)
518.781 Million cell updates/sec

itle: US-10-553-509-11
erfect score: 16
equence: 1 catcgcctggactccg 16

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 1403666 seqs, 935554401 residues

otal number of hits satisfying chosen parameters: 1475510

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
c 1	16	100.0	17	2	US-08-446-530-5	Sequence 5, Appli
2	16	100.0	17	2	US-08-446-530-7	Sequence 7, Appli
c 3	16	100.0	17	2	US-09-097-562-5	Sequence 5, Appli
4	16	100.0	17	2	US-09-097-562-7	Sequence 7, Appli
5	15.6	100.0	21	3	US-09-657-472-1650	Sequence 1650, Ap

!--StartFragment-->RESULT 1
3-08-446-530-5/c
Sequence 5, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,530
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-446-530-5

Query Match 100.0%; Score 16; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCG 16
||||||||||||||||
o 17 CATCGCCTGGACTCCG 2

ESULT 2
3-08-446-530-7
Sequence 7, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,530
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-446-530-7

Query Match 100.0%; Score 16; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCG 16
||||||||||||||||
o 1 CATCGCCTGGACTCCG 16

ESULT 3
3-09-097-562-5/c
Sequence 5, Application US/09097562
Patent No. 5877283
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,530
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-09-097-562-5

Query Match 100.0%; Score 16; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCG 16
||||||||||||||||
o 17 CATCGCCTGGACTCCG 2

ESULT 4
3-09-097-562-7
Sequence 7, Application US/09097562
Patent No. 5877283
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,530
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-09-097-562-7

Query Match 100.0%; Score 16; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCG 16
||||||||||||||||
o 1 CATCGCCTGGACTCCG 16

!--EndFragment-->

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104105_us-10-553-509-12.szlm60.rni.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104105_us-10-53-509-12.szlm60.rni.

tart

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 06:40:47 ; Search time 54.1011 Seconds
(without alignments)
518.781 Million cell updates/sec

itle: US-10-553-509-12
erfect score: 15
equence: 1 catcgcctggactcc 15

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 1403666 seqs, 935554401 residues

otal number of hits satisfying chosen parameters: 1475510

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
c 1	15	100.0	17	2	US-08-446-530-5	Sequence 5, Appli
2	15	100.0	17	2	US-08-446-530-7	Sequence 7, Appli
c 3	15	100.0	17	2	US-09-097-562-5	Sequence 5, Appli
4	15	100.0	17	2	US-09-097-562-7	Sequence 7, Appli
5	14.6	100.0	21	3	US-09-657-472-1650	Sequence 1650, Ap

	8	13.4	89.3	17	2	US-08-446-530-8	Sequence 8, Appli
c	9	13.4	89.3	17	2	US-09-097-562-6	Sequence 6, Appli
	10	13.4	89.3	17	2	US-09-097-562-8	Sequence 8, Appli
	11	13.4	89.3	33	2	US-08-646-367-19	Sequence 19, Appl
	12	13.4	89.3	35	3	US-09-269-332-21	Sequence 21, Appl
	13	13.4	89.3	39	2	US-08-478-039-44	Sequence 44, Appl
	14	13.4	89.3	39	2	US-08-476-349A-44	Sequence 44, Appl
	15	13.4	89.3	39	3	US-08-523-894-37	Sequence 37, Appl
	16	13.4	89.3	57	2	US-07-960-982-22	Sequence 22, Appl
	17	12.6	84.0	21	3	US-09-657-472-1651	Sequence 1651, Ap
	18	12.6	84.0	33	3	US-09-592-998C-4	Sequence 4, Appli
	19	12.6	84.0	34	3	US-09-019-441A-15	Sequence 15, Appl
	20	12.6	84.0	34	5	US-09-292-053A-11	Sequence 11, Appl
c	21	12.4	82.7	50	3	US-10-131-827-1981	Sequence 1981, Ap
c	22	12.4	82.7	50	5	US-10-131-831-1981	Sequence 1981, Ap
c	23	11.8	78.7	18	2	US-09-213-767-17	Sequence 17, Appl
	24	11.8	78.7	25	3	US-09-396-196G-21494	Sequence 21494, A
	25	11.8	78.7	25	3	US-09-396-196G-28279	Sequence 28279, A
	26	11.8	78.7	25	3	US-09-396-196G-28280	Sequence 28280, A
	27	11.8	78.7	25	3	US-09-396-196G-28281	Sequence 28281, A
c	28	11.8	78.7	25	3	US-09-396-196G-94211	Sequence 94211, A
	29	11.8	78.7	29	2	US-08-646-367-20	Sequence 20, Appl
	30	11.8	78.7	35	3	US-08-814-412-25	Sequence 25, Appl
	31	11.8	78.7	35	7	PCT-US94-14106-27	Sequence 27, Appl
	32	11.8	78.7	39	2	US-08-478-039-42	Sequence 42, Appl
	33	11.8	78.7	39	2	US-08-476-349A-42	Sequence 42, Appl
	34	11.8	78.7	39	3	US-08-523-894-35	Sequence 35, Appl
	35	11.8	78.7	45	2	US-08-761-277A-74	Sequence 74, Appl
c	36	11.8	78.7	49	2	US-07-960-982-23	Sequence 23, Appl
	37	11.4	76.0	16	2	US-08-311-760A-391	Sequence 391, App
	38	11.4	76.0	16	2	US-08-774-310-391	Sequence 391, App
c	39	11.4	76.0	20	2	US-08-450-905B-140	Sequence 140, App
c	40	11.4	76.0	20	3	US-07-982-759F-140	Sequence 140, App
	41	11.4	76.0	24	2	US-08-467-264-8	Sequence 8, Appli
	42	11.4	76.0	25	3	US-08-469-260A-655	Sequence 655, App
	43	11.4	76.0	25	3	US-08-469-260A-698	Sequence 698, App
	44	11.4	76.0	25	3	US-08-488-446-655	Sequence 655, App
	45	11.4	76.0	25	3	US-08-488-446-698	Sequence 698, App

ALIGNMENTS

ESULT 1
3-08-446-530-5/c
Sequence 5, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,530
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-446-530-5

Query Match 100.0%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15
||||||||||||||||
D 17 CATCGCCTGGACTCC 3

ESULT 2
3-08-446-530-7
Sequence 7, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,530
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-446-530-7

Query Match 100.0%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
y          1 CATCGCCTGGACTCC 15
             |||||||||||||||
o          1 CATCGCCTGGACTCC 15
```

ESULT 3
3-09-097-562-5/c
Sequence 5, Application US/09097562
Patent No. 5877283
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,530
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-09-097-562-5

Query Match 100.0%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
y          1 CATCGCCTGGACTCC 15
             |||||||||||||||
o         17 CATCGCCTGGACTCC 3
```

ESULT 4
3-09-097-562-7
Sequence 7, Application US/09097562
Patent No. 5877283
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,530
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
S-09-097-562-7

Query Match 100.0%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCC 15
||||||||||||||
D 1 CATCGCCTGGACTCC 15

ESULT 5
S-09-657-472-1650
Sequence 1650, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1650
LENGTH: 21
TYPE: DNA

ORGANISM: Homo sapiens
3-09-657-472-1650

Query Match 100.0%; Score 15; DB 3; Length 21;
Best Local Similarity 93.3%; Pred. No. 92;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCC 15
||||||:|||||||
o 4 CATCGCCYGGACTCC 18

ESULT 6
3-09-304-232-896
Sequence 896, Application US/09304232
Patent No. 6525185
GENERAL INFORMATION:
APPLICANT: Fan, Jian Bing
APPLICANT: Chakravarti, Aravinda
APPLICANT: Halushka, Marc Kenneth
APPLICANT: Case Western Reserve University School of Medicine
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Polymorphisms Associated With
TITLE OF INVENTION: Hypertension
FILE REFERENCE: 018547-034210US
CURRENT APPLICATION NUMBER: US/09/304,232
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: US 60/084,641
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 909
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 896
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ADRB3EX1 416
3-09-304-232-896

Query Match 100.0%; Score 15; DB 3; Length 29;
Best Local Similarity 93.3%; Pred. No. 94;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCC 15
||||||:|||||||
o 8 CATCGCCYGGACTCC 22

ESULT 7
3-08-446-530-6/c
Sequence 6, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104100_us-10-553-509-8.szlm60.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104100_us-10-53-509-8.szlm60.rng.

tart | next page

Go Back to previous pag

```
                        GenCore version 5.1.9
                  Copyright (c) 1993 - 2006  Biocceleration Ltd.


M nucleic - nucleic search, using sw model

un on:          December 15, 2006, 05:57:43 ; Search time 241.124 Seconds
                                           (without alignments)
                                           578.313 Million cell updates/sec

itle:           US-10-553-509-8
erfect score:   20
equence:        1 cgtggccatcgcccggactc 20

coring table:   IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

earched:        5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters:      5397982

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase :       N_Geneseq_8*:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

                 %
esult            Query
  No.    Score   Match Length DB  ID                          Description
---------------------------------------------------------------------------
```

	3	20	100.0	34	13	ADT93454	Adt93454 Human bet
	4	20	100.0	41	6	ABK50104	Abk50104 Sense str
	5	19.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
	6	19.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
C	7	19	95.0	25	4	AAC89164	Aac89164 Sample DN
	8	19	95.0	25	12	ADO26526	Ado26526 Novel hyb
	9	18.4	92.0	34	13	ADT93453	Adt93453 Human bet
	10	18	90.0	20	14	AEC91759	Aec91759 Probe 5T-
	11	17.4	87.0	25	12	ADO26525	Ado26525 Novel hyb
	12	17	85.0	21	14	AEC91760	Aec91760 Probe 3T-
	13	17	85.0	27	3	AAA73177	Aaa73177 Beta-3-ad
	14	16.6	83.0	21	3	AAC73164	Aac73164 SNP flank
	15	16.4	82.0	25	6	ABL40568	Abl40568 Primer #8
	16	16.4	82.0	26	6	ABL40567	Abl40567 Primer #7
	17	15.4	77.0	21	4	AAF96885	Aaf96885 Human gen
	18	15.4	77.0	27	3	AAA73176	Aaa73176 Beta-3-ad
	19	15	75.0	16	13	ADT93445	Adt93445 Fluoresce
	20	15	75.0	19	13	ADT93446	Adt93446 Fluoresce
C	21	14.8	74.0	20	4	AAF31792	Aaf31792 Human RAN
	22	14.4	72.0	19	6	ABK50102	Abk50102 Allele sp
C	23	14.2	71.0	60	6	ABN47900	Abn47900 Human spl
C	24	14	70.0	17	2	AAT58988	Aat58988 Obesity a
	25	14	70.0	17	2	AAT58990	Aat58990 Obesity a
	26	14	70.0	17	15	AEE87557	Aee87557 Human min
	27	14	70.0	19	13	ADT93447	Adt93447 Fluoresce
	28	14	70.0	20	14	AED47650	Aed47650 Human bet
	29	14	70.0	25	13	ADR55076	Adr55076 Drug ther
	30	14	70.0	41	2	AAV13420	Aav13420 R64 allel
	31	14	70.0	41	3	AAA73179	Aaa73179 Beta-3-ad
C	32	13.8	69.0	42	7	ADI92927	Adi92927 Thermus s
	33	13.6	68.0	20	12	ADM15299	Adm15299 Human mPG
C	34	13.6	68.0	36	12	ADL24391	Adl24391 Multiple
C	35	13.6	68.0	36	12	ADL24405	Adl24405 Multiple
C	36	13.6	68.0	51	4	AAI79557	Aai79557 Human sil
	37	13.6	68.0	54	6	AAD37446	Aad37446 Human nec
	38	13.4	67.0	15	6	ABK50103	Abk50103 Oligonucl
	39	13.4	67.0	20	10	ADC51219	Adc51219 Oligonucl
	40	13.4	67.0	20	10	ADF55593	Adf55593 Oligonucl
	41	13.4	67.0	20	12	ADQ67903	Adq67903 Beta-3-ad
C	42	13.4	67.0	30	4	AAF44557	Aaf44557 Mouse DSS
	43	13.4	67.0	32	15	AEF10675	Aef10675 Aspergill
C	44	13.4	67.0	48	4	AAH97483	Aah97483 Human Chk
C	45	13.4	67.0	48	5	ADV61702	Adv61702 HBV amber

ALIGNMENTS

ESULT 1
DT93448
D ADT93448 standard; DNA; 20 BP.
K
C ADT93448;
K
T 13-JAN-2005 (first entry)
K
E Fluorescent probe targeted to human B3AR C190 variant DNA - SEQ ID 8.
K
W SNP detection; beta3 adrenaline receptor; ss; probe.
K
S Homo sapiens.
K
H Key Location/Qualifiers
T modified_base 20
T /*tag= a
T /mod_base= OTHER
T /note= "OTHER = Linked to TAMRA group"
K
N WO2004092385-A1.

XX
PF 16-APR-2004; 2004WO-JP005525.
XX
PR 18-APR-2003; 2003JP-00114381.
XX
PA (ARKR-) ARKRAY INC.
XX
PI Hirai M;
XX
DR WPI; 2004-784610/77.
XX
PT Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT receptor gene having single nucleotide polymorphism, labeled at terminal
PT with fluorescent dye and shows decrease in fluorescence of fluorescent
PT dye upon hybridization.
XX
PS Claim 2; SEQ ID NO 8; 31pp; Japanese.
XX
CC The invention relates to a novel nucleic acid probe which is labelled at
CC a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC of the fluorescent dye is observed upon hybridisation. The probe
CC comprises a base sequence derived from a fully defined sequence of 1227
CC nucleotides as given in the specification and being labelled at the 3' or
CC 5' end with a fluorescent dye. The probe of the invention may be useful
CC for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC contamination of the amplified product is prevented and the process is
CC automated. The current sequence is that of the fluorescent-labelled probe
CC (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC receptor (B3AR) C190 variant DNA.
XX
SQ Sequence 20 BP; 2 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

 Query Match   100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity   100.0%; Pred. No. 13;
 Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGTGGCCATCGCCCGGACTC 20
              ||||||||||||||||||||
Db   1 CGTGGCCATCGCCCGGACTC 20

RESULT 2
AEC91741
ID AEC91741 standard; DNA; 20 BP.
XX
AC AEC91741;
XX
DT 01-DEC-2005 (first entry)
XX
DE Primer 3CB-B3AR-mt-F2-20 SEQ ID NO:17.
XX
KW DNA detection; SNP detection; primer; ss.
XX
OS Synthetic.
XX
PN JP2005261354-A.
XX
PD 29-SEP-2005.
XX
PF 19-MAR-2004; 2004JP-00080974.
XX
PR 19-MAR-2004; 2004JP-00080974.
XX
PA (KYOT-) KYOTO DAIICHI KAGAKU KK.
XX
PI Inose K;
XX
DR WPI; 2005-662138/68.

DT Detecting target nucleic acid, involves detecting target based on change
DT of fluorescence intensity due to formation or dissociation of hybrid of
DT target nucleic acid and hybridization probe having 5-carboxy fluorescein.
XX
DE Example 6; SEQ ID NO 17; 28pp; Japanese.
XX
CC The invention relates to a method (M1) for detecting a target nucleic
CC acid. (M1) involves measuring the change of fluorescence intensity due to
CC formation or dissociation of the hybrid of the hybridization probe
CC comprising a labeled terminal portion, and a target nucleic acid, and
CC detecting the target nucleic acid based on the change, where the
CC hybridization probe is labeled using the fluorescent pigment chosen from
CC 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
CC -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
CC dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
CC 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
CC hydrazide (Cascade blue). Also described: (1) a real-time PCR method
CC (M2), which involves carrying out real-time PCR using the hybridization
CC probe labeled with the fluorescent pigment, where the hybridization probe
CC is the probe labeled at its terminal with the fluorescent pigment chosen
CC from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
CC curve analysis (M3), which involves using the hybridization probe labeled
CC with the fluorescent pigment, where the hybridization probe is the probe
CC labeled at its terminal with the fluorescent pigment chosen from TAMRA,
CC BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
CC target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
CC target nucleic acid and single nucleotide polymorphisms (SNPs), and in
CC measurement of the ratio of normal type DNA and variant DNA. (M1) enables
CC detection of the nucleic acid by fluorescent detection method, easily and
CC cost effectively. The present sequence represents a primer used in an
CC example from the present invention.
XX
SQ Sequence 20 BP; 2 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGGCCATCGCCCGGACTC 20
||||||||||||||||||||
Db 1 CGTGGCCATCGCCCGGACTC 20

RESULT 3
ADT93454
ID ADT93454 standard; DNA; 34 BP.
XX
AC ADT93454;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human beta3 adrenaline receptor (B3AR) C190 variant DNA fragment.
XX
KW single nucleotide polymorphism; SNP; SNP detection;
KW beta3 adrenaline receptor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(19,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX
PN WO2004092385-A1.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-JP005525.
XX
PR 18-APR-2003; 2003JP-00114381

A (ARKR-) ARKRAY INC.
X
I Hirai M;
X
R WPI; 2004-784610/77.
X
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline
T receptor gene having single nucleotide polymorphism, labeled at terminal
T with fluorescent dye and shows decrease in fluorescence of fluorescent
T dye upon hybridization.
X
S Example 1; Fig 1; 31pp; Japanese.
X
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the human beta3 adrenaline
C receptor (B3AR) C190 variant DNA fragment of the invention.
X
Q Sequence 34 BP; 5 A; 14 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGTGGCCATCGCCCGGACTC 20
  ||||||||||||||||||||
D 6 CGTGGCCATCGCCCGGACTC 25

ESULT 4
3K50104
D ABK50104 standard; DNA; 41 BP.
X
C ABK50104;
X
T 15-JUL-2002 (first entry)
X
E Sense strand of target nucleic acid.
X
W Optimal reagent oligonucleotide; target nucleic acid evaluation;
W target feature; exclusion value; ranking value; sequence window;
W single nucleotide polymorphism; SNP; ds.
X
S Synthetic.
X
H Key Location/Qualifiers
T variation replace(21,T)
T /*tag= a
T /standard_name= "Single nucleotide polymorphism"
X
N WO200229379-A2.
X
D 11-APR-2002.
X
F 04-OCT-2001; 2001WO-US031037.
X
R 04-OCT-2000; 2000US-0237383P.
X
A (CELA-) CELADON LAB INC.
X
I Peterson RJ;

XX
PT Determining an optimal reagent oligonucleotide for evaluating a target
PT nucleic acid having a target feature, involves defining a set of
PT exclusion values and/or ranking values specific to a biochemical method.
XX
PS Example; Fig 4A; 91pp; English.
XX
CC The present invention relates to a new method for determining an optimal
CC reagent oligonucleotide for evaluating a target nucleic acid having a
CC target feature. The method comprises defining a set of exclusion values
CC and/or ranking values specific to the method, defining a sequence window
CC adjacent to the target, and generating candidate reagent oligonucleotides
CC complementary to the sense and/or antisense strands of the target within
CC the window. The method can be used for determining an optimal reagent
CC oligonucleotide sequence for use in a biochemical method for evaluating a
CC target nucleic acid sequence having a target feature. The present nucleic
CC acid sequence represent the sense strand of a target nucleic acid. This
CC sequence was used in the methods of the invention in a sequence window
XX
SQ Sequence 41 BP; 7 A; 16 C; 11 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGGCCATCGCCCGGACTC 20
||||||||||||||||||||
Db 8 CGTGGCCATCGCCCGGACTC 27

RESULT 5
AAA04696
ID AAA04696 standard; DNA; 29 BP.
XX
AC AAA04696;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene ADRB3.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
KW polycystic kidney disease; von Willebrands disease; forensic; human;
KW tuberous sclerosis; hereditary hemorrhagica telangiectasia;
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW Ehlers-Danlos syndrome; ss.
XX
OS Homo sapiens.
XX
PN EP955382-A2.
XX
PD 10-NOV-1999.
XX
PF 07-MAY-1999; 99EP-00250150.
XX
PR 07-MAY-1998; 98US-0084641P.
PR 03-MAY-1999; 99US-00304232.
XX
PA (AFFY-) AFFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Fan JB, Chakravarti A, Haluska MK;
XX
DR WPI; 2000-107928/10.
XX
PT Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.
XX
CC Disclosure; Page 45; 53pp; English.

C The invention provides polymorphic fragments of genes associated with
C hypertension. The nucleic acids including the polymorphic sites can be
C used as probes or primers for expressing variant proteins. Detection of
C the polymorphisms is useful in designing prophylactic and therapeutic
C regimes customized to underlying abnormalities. The polymorphisms can be
C used for association studies for hypertension, and in hypertension
C diagnostic assays. Where the polymorphisms have strong correlation with
C hypertension, within a gene, they are likely to have a causative role in
C hypertension. This information can be used to find the precise role of a
C polymorphism in the disease, and this can be used to identify potential
C drugs which combat the disease. The polymorphisms can be tested for
C association with other diseases e.g. agammaglobulinemia, diabetes
C insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
C syndrome, Fabrys disease, familial hypercholesterolemia, polycystic
C kidney disease, hereditary spherocytosis, von Willebrands disease,
C tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
C colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
C acute intermittent porphyria. The polymorphic forms can also be used in
C forensics to identify individuals
XX
SQ Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 3; Length 29;
Best Local Similarity 95.0%; Pred. No. 21;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGTGGCCATCGCCCGGACTC 20
||||||||||||||:||||||
D 2 CGTGGCCATCGCCYGGACTC 21

ESULT 6
BK50101
D ABK50101 standard; DNA; 41 BP.
XX
C ABK50101;
XX
R 15-JUL-2002 (first entry)
XX
E Nucleic acid sequence used for sequence formatting.
XX
W Optimal reagent oligonucleotide; target nucleic acid evaluation;
W target feature; exclusion value; ranking value; sequence window;
W sequence formatting; ds.
XX
S Synthetic.
XX
N WO200229379-A2.
XX
D 11-APR-2002.
XX
F 04-OCT-2001; 2001WO-US031037.
XX
R 04-OCT-2000; 2000US-0237383P.
XX
A (CELA-) CELADON LAB INC.
XX
I Peterson RJ;
XX
R WPI; 2002-340129/37.
XX
P Determining an optimal reagent oligonucleotide for evaluating a target
P nucleic acid having a target feature, involves defining a set of
P exclusion values and/or ranking values specific to a biochemical method.
XX
S Example; Fig 1B; 91pp; English.
XX
C The present invention relates to a new method for determining an optimal
C reagent oligonucleotide for evaluating a target nucleic acid having a
C target feature. The method comprises defining a set of exclusion values

and/or running values specific to the method, defining a sequence window
adjacent to the target, and generating candidate reagent oligonucleotides
complementary to the sense and/or antisense strands of the target within
the window. The method can be used for determining an optimal reagent
oligonucleotide sequence for use in a biochemical method for evaluating a
target nucleic acid sequence having a target feature. The present nucleic
acid sequence represent a DNA molecule used in the methods of the
invention for nucleic acid sequence formatting
XX
Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 6; Length 41;
Best Local Similarity 95.0%; Pred. No. 20;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGTGGCCATCGCCCGGACTC 20
||||||||||||:||||||
C 8 CGTGGCCATCGCCYGGACTC 27

ESULT 7
AC89164/c
AAC89164 standard; DNA; 25 BP.
XX
AAC89164;
XX
08-MAR-2001 (first entry)
XX
Sample DNA #2 used in a method for gene analysis.
XX
Gene analysis; infectious disease; genetic disease; gene expression; ss.
XX
Unidentified.
XX
Key Location/Qualifiers
modified_base 1
/*tag= a
/mod_base= OTHER
/note= "OTHER = CY5 labelled A"
XX
EP1055735-A2.
XX
29-NOV-2000.
XX
25-MAY-2000; 2000EP-00110932.
XX
25-MAY-1999; 99JP-00144749.
XX
(MITU) MITSUBISHI CHEM CORP.
XX
Hatakeyama K;
XX
WPI; 2001-042414/06.
XX
A method for gene analysis, e.g. for gene diagnosis of infectious or
genetic diseases, by detecting hybridization between a nucleic acid probe
and sample in the presence of a double-stranded DNA-binding protein.
XX
Example 2; Page 10; 18pp; English.
XX
The present invention relates to a method for gene analysis. The method
comprises detecting hybridisation, which is caused in the presence of a
double-stranded DNA-binding protein, between a probe nucleic acid and a
sample nucleic acid. The method is useful for gene analysis, particularly
in determining the nucleotide sequence of nucleic acids, in gene
diagnosis of infectious or genetic diseases, or monitoring of genome DNA
expression. The present sequence is a sample DNA used in the method of
the present invention
XX
Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          2 GTGGCCATCGCCCGGACTC 20
             ||||||||||||||||||
D         25 GTGGCCATCGCCCGGACTC 7
```

ESULT 8
DO26526
D ADO26526 standard; DNA; 25 BP.
K
C ADO26526;
K
R 12-AUG-2004 (first entry)
K
E Novel hybridisation detection-related oligonucleotide SeqID2.
K
W hybridisation detection; immobilised probe; AC impedance;
W foetal genome analysis; ss.
K
S Unidentified.
K
N WO2004044570-A1.
K
D 27-MAY-2004.
K
F 30-SEP-2003; 2003WO-JP012499.
K
R 14-NOV-2002; 2002JP-00331059.
K
A (TOYA-) TOYAMA PREFECTURE.
A (COSE-) COSEL CO LTD.
A (TATE-) TATEYAMA KAGAKU IND CO LTD.
A (TOXX) TOYO KAKO CO LTD.
K
I Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
I Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
K
R WPI; 2004-420427/39.
K
T Detection of hybridization of an immobilized probe to a target nucleic
T acid by measuring AC impedance across the carrier surface for specific
T gene detection in investigation and diagnosis of disease.
K
S Example; SEQ ID NO 2; 33pp; Japanese.
K
C This invention relates to a novel method of detecting hybridisation of an
C immobilised probe to a target nucleic acid using measurement of AC
C impedance. Detection of specific genes and gene sequences in nucleic acid
C samples (such as samples of genomic DNA) may be useful for diagnosis,
C prediction and prevention of genetic disorders and analysis of foetal
C genome. Hybridisation is detected with high accuracy and sensitivity
C without the use of dyes. The present sequence is that of an
C oligonucleotide which was used in the exemplification of the invention.
K
Q Sequence 25 BP; 4 A; 10 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          2 GTGGCCATCGCCCGGACTC 20
             ||||||||||||||||||
D          1 GTGGCCATCGCCCGGACTC 19
```

ESULT 9
DT93453
D ADT93453 standard; DNA; 24 BP

ID   ADT93453;
XX
DT   13-JAN-2005 (first entry)
XX
DE   Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.
XX
KW   single nucleotide polymorphism; SNP; SNP detection;
KW   beta3 adrenaline receptor; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   replace(19,C)
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO2004092385-A1.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-JP005525.
XX
PR   18-APR-2003; 2003JP-00114381.
XX
PA   (ARKR-) ARKRAY INC.
XX
PI   Hirai M;
XX
DR   WPI; 2004-784610/77.
XX
PT   Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT   receptor gene having single nucleotide polymorphism, labeled at terminal
PT   with fluorescent dye and shows decrease in fluorescence of fluorescent
PT   dye upon hybridization.
XX
PS   Example 1; Fig 1; 31pp; Japanese.
XX
CC   The invention relates to a novel nucleic acid probe which is labelled at
CC   a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC   of the fluorescent dye is observed upon hybridisation. The probe
CC   comprises a base sequence derived from a fully defined sequence of 1227
CC   nucleotides as given in the specification and being labelled at the 3' or
CC   5' end with a fluorescent dye. The probe of the invention may be useful
CC   for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC   beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC   detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC   contamination of the amplified product is prevented and the process is
CC   automated. The current sequence is that of the human beta3 adrenaline
CC   receptor (B3AR) T190 variant DNA fragment of the invention.
XX
SQ   Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

 Query Match   92.0%; Score 18.4; DB 13; Length 34;
 Best Local Similarity   95.0%; Pred. No. 74;
 Matches   19; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Y   1 CGTGGCCATCGCCCGGACTC 20
             |||||||||||| ||||||
D   6 CGTGGCCATCGCCTGGACTC 25

ESULT 10
EC91759
ID   AEC91759 standard; DNA; 20 BP.
XX
AC   AEC91759;
XX
DT   01-DEC-2005 (first entry)
XX
DE   Probe 5T_B3AR_m_IMS_E1_20_SEQ_ID_NO:35

KW DNA detection; SNP detection; probe; ss.
XX
OS Synthetic.
XX
PN JP2005261354-A.
XX
PD 29-SEP-2005.
XX
PF 19-MAR-2004; 2004JP-00080974.
XX
PR 19-MAR-2004; 2004JP-00080974.
XX
PA (KYOT-) KYOTO DAIICHI KAGAKU KK.
XX
PI Inose K;
XX
DR WPI; 2005-662138/68.
XX
PT Detecting target nucleic acid, involves detecting target based on change
PT of fluorescence intensity due to formation or dissociation of hybrid of
PT target nucleic acid and hybridization probe having 5-carboxy fluorescein.
XX
PS Example 10; SEQ ID NO 35; 28pp; Japanese.
XX
CC The invention relates to a method (M1) for detecting a target nucleic
CC acid. (M1) involves measuring the change of fluorescence intensity due to
CC formation or dissociation of the hybrid of the hybridization probe
CC comprising a labeled terminal portion, and a target nucleic acid, and
CC detecting the target nucleic acid based on the change, where the
CC hybridization probe is labeled using the fluorescent pigment chosen from
CC 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
CC -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
CC dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
CC 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
CC hydrazide (Cascade blue). Also described: (1) a real-time PCR method
CC (M2), which involves carrying out real-time PCR using the hybridization
CC probe labeled with the fluorescent pigment, where the hybridization probe
CC is the probe labeled at its terminal with the fluorescent pigment chosen
CC from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
CC curve analysis (M3), which involves using the hybridization probe labeled
CC with the fluorescent pigment, where the hybridization probe is the probe
CC labeled at its terminal with the fluorescent pigment chosen from TAMRA,
CC BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
CC target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
CC target nucleic acid and single nucleotide polymorphisms (SNPs), and in
CC measurement of the ratio of normal type DNA and variant DNA. (M1) enables
CC detection of the nucleic acid by fluorescent detection method, easily and
CC cost effectively. The present sequence represents a probe used in an
CC example from the present invention.
XX
SQ Sequence 20 BP; 2 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

 Query Match   90.0%; Score 18; DB 14; Length 20;
 Best Local Similarity   100.0%; Pred. No. 1.1e+02;
 Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGTGGCCATCGCCCGGAC 18
              ||||||||||||||||||
Db   3 CGTGGCCATCGCCCGGAC 20

RESULT 11
ADO26525
ID ADO26525 standard; DNA; 25 BP.
XX
AC ADO26525;
XX
DT 12-AUG-2004 (first entry)
XX
DE Novel hybridisation detection related oligonucleotide SeqID1

KW   hybridisation detection; immobilised probe; AC impedance;
KW   foetal genome analysis; ss.
XX
OS   Unidentified.
XX
PN   WO2004044570-A1.
XX
PD   27-MAY-2004.
XX
PF   30-SEP-2003; 2003WO-JP012499.
XX
PR   14-NOV-2002; 2002JP-00331059.
XX
PA   (TOYA-) TOYAMA PREFECTURE.
PA   (COSE-) COSEL CO LTD.
PA   (TATE-) TATEYAMA KAGAKU IND CO LTD.
PA   (TOXX) TOYO KAKO CO LTD.
XX
PI   Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
PI   Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
XX
DR   WPI; 2004-420427/39.
XX
PT   Detection of hybridization of an immobilized probe to a target nucleic
PT   acid by measuring AC impedance across the carrier surface for specific
PT   gene detection in investigation and diagnosis of disease.
XX
PS   Example; SEQ ID NO 1; 33pp; Japanese.
XX
CC   This invention relates to a novel method of detecting hybridisation of an
CC   immobilised probe to a target nucleic acid using measurement of AC
CC   impedance. Detection of specific genes and gene sequences in nucleic acid
CC   samples (such as samples of genomic DNA) may be useful for diagnosis,
CC   prediction and prevention of genetic disorders and analysis of foetal
CC   genome. Hybridisation is detected with high accuracy and sensitivity
CC   without the use of dyes. The present sequence is that of an
CC   oligonucleotide which was used in the exemplification of the invention.
XX
SQ   Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

 Query Match   87.0%; Score 17.4; DB 12; Length 25;
 Best Local Similarity   94.7%; Pred. No. 2.1e+02;
 Matches   18; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   2 GTGGCCATCGCCCGGACTC 20
              ||||||||||| ||||||
Db   1 GTGGCCATCGCCTGGACTC 19

RESULT 12
AEC91760
ID   AEC91760 standard; DNA; 21 BP.
XX
AC   AEC91760;
XX
DT   01-DEC-2005 (first entry)
XX
DE   Probe 3T-B3AR-w-IMS-F2-21 SEQ ID NO:36.
XX
KW   DNA detection; SNP detection; probe; ss.
XX
OS   Synthetic.
XX
PN   JP2005261354-A.
XX
PD   29-SEP-2005.
XX
PF   19-MAR-2004; 2004JP-00080974.
XX
PR   19-MAR-2004; 2004JP-00080974.

A (KYOT-) KYOTO DAIICHI KAGAKU KK.
X
I Inose K;
X
R WPI; 2005-662138/68.
X
T Detecting target nucleic acid, involves detecting target based on change
T of fluorescence intensity due to formation or dissociation of hybrid of
T target nucleic acid and hybridization probe having 5-carboxy fluorescein.
X
S Example 10; SEQ ID NO 36; 28pp; Japanese.
X
C The invention relates to a method (M1) for detecting a target nucleic
C acid. (M1) involves measuring the change of fluorescence intensity due to
C formation or dissociation of the hybrid of the hybridization probe
C comprising a labeled terminal portion, and a target nucleic acid, and
C detecting the target nucleic acid based on the change, where the
C hybridization probe is labeled using the fluorescent pigment chosen from
C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
C 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
C hydrazide (Cascade blue). Also described: (1) a real-time PCR method
C (M2), which involves carrying out real-time PCR using the hybridization
C probe labeled with the fluorescent pigment, where the hybridization probe
C is the probe labeled at its terminal with the fluorescent pigment chosen
C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
C curve analysis (M3), which involves using the hybridization probe labeled
C with the fluorescent pigment, where the hybridization probe is the probe
C labeled at its terminal with the fluorescent pigment chosen from TAMRA,
C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
C target nucleic acid and single nucleotide polymorphisms (SNPs), and in
C measurement of the ratio of normal type DNA and variant DNA. (M1) enables
C detection of the nucleic acid by fluorescent detection method, easily and
C cost effectively. The present sequence represents a probe used in an
C example from the present invention.
X
Q Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 4 GGCCATCGCCCGGACTC 20
  ||||||||||||||||
D 1 GGCCATCGCCCGGACTC 17

ESULT 13
AA73177
D AAA73177 standard; DNA; 27 BP.
X
C AAA73177;
X
T 28-NOV-2000 (first entry)
X
E Beta-3-adrenergic receptor R64 allele oligonucleotide SEQ ID NO:39.
X
W Amplification; target; hairpin; primer; blocking oligonucleotide; donor;
W acceptor; detection; telomerase activity; triamplification; PCR;
W allele-specific PCR; nucleic acid sequence-based amplification;
W strand displacement amplification; telomeric repeat amplification;
W cascade rolling circle amplification; in situ amplification;
W amplification refractory mutation system; ss.
X
S Unidentified.
X
N US6090552-A.

XX
PF 11-JUL-1997; 97US-00891516.
XX
PR 16-JUL-1996; 96US-00683667.
PR 03-JAN-1997; 97US-00778487.
PR 11-APR-1997; 97US-00837034.
XX
PA (INTE-) INTERGEN CO.
XX
PI Hohman RJ, Winn-Deen ES, Bhatnagar SK, Nazarenko IA;
XX
DR WPI; 2000-505149/45.
XX
DT Use of labeled hairpin amplification oligonucleotides to detect
DT telomerase activity and to determine the presence of target nucleic acid
DT sequence in a sample.
XX
CC Example 10; Col 56; 98pp; English.
XX
CC The present invention describes the use of labelled hairpin amplification
CC oligonucleotides to detect telomerase activity and to determine the
CC presence of target nucleic acid sequence in a sample. The method can be
CC used to detect telomerase activity and to determine the presence of
CC target nucleic acid sequences in a sample and for detecting amplification
CC products of polymerase chain reaction, allele-specific polymerase chain
CC reaction, triamplification, nucleic acid sequence-based amplification,
CC strand displacement amplification, telomeric repeat amplification,
CC cascade rolling circle amplification, amplification refractory mutation
CC system or in situ amplification. The use of a universal hairpin primer
CC permits a closed tube format. Amplification and detection are performed
CC in the same tube so that no carry-over contamination with amplicon occurs
CC and consequently no false positive results are obtained. The present
CC sequence represents an oligonucleotide which is used in the
CC exemplification of the present invention
XX
SQ Sequence 27 BP; 3 A; 9 C; 9 G; 6 T; 0 U; 0 Other;

 Query Match   85.0%; Score 17; DB 3; Length 27;
 Best Local Similarity   100.0%; Pred. No. 3.3e+02;
 Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGTGGCCATCGCCCGGA 17
              |||||||||||||||||
Db   11 CGTGGCCATCGCCCGGA 27

RESULT 14
AAC73164
ID AAC73164 standard; DNA; 21 BP.
XX
AC AAC73164;
XX
DT 02-FEB-2001 (first entry)
XX
DE SNP flanking sequence #24 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.

A (AFFY-) AFFYMETRIX INC.
X
I Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
I Ryder T, Sklar P;
X
R WPI; 2000-656171/63.
X
P Universal array of oligonucleotides tags attached to a solid substrate
P along with locus-specific tagged oligonucleotides useful in genotyping
P using single base extension reactions.
X
S Example 7; Page 50; 70pp; English.
X
C The present invention relates to an oligonucleotide array comprising
C oligonucleotide tags fixed to a solid substrate. The oligonucleotide
C array is useful for genotyping a nucleic acid sample at one or more loci
C via single base extension (SBE) reactions. A pair of primers is used to
C amplify a polymorphic locus in a sample e.g. a single nucleotide
C polymorphism (SNP). The present sequence is one such polymorphic locus
C used in the present invention. The amplified nucleic acid product is then

tart | next page

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104357_us-10-553-509-2_copy_165_200.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104357_us-10-53-509-2_copy_165_200.rng.

tart | next page

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 14:32:10 ; Search time 177.031 Seconds
(without alignments)
1417.837 Million cell updates/sec

itle: US-10-553-509-2_COPY_165_200
erfect score: 36
equence: 1 cctgctggtcatcgtggccatcgcccggactccgag 36

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters: 10489840

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	36	100.0	100	14	AEG01748	Template

2	36	100.0	210	2	[illegible]	[illegible] Human bia
3	36	100.0	1227	13	ADT93442	Adt93442 Human bet
4	35.6	100.0	210	2	AAX11762	Aax11762 Human bia
5	35.6	100.0	420	14	AEC91757	Aec91757 Template
6	35.6	100.0	2040	6	ABK11513	Abk11513 Human bet
7	35.6	100.0	5669	14	ADZ42281	Adz42281 Human bet
8	35.6	100.0	10306	6	ABK11451	Abk11451 Human bet
9	34.4	95.6	1003	12	ACH91802	Ach91802 Human gen
10	34.4	95.6	1185	6	ABX13060	Abx13060 Human bet
11	34.4	95.6	1185	14	AEA13746	Aea13746 Human bet
12	34.4	95.6	1227	2	AAQ55693	Aaq55693 DNA encod
13	34.4	95.6	1227	13	ADT93441	Adt93441 Human bet
14	34.4	95.6	1270	10	ACA56586	Aca56586 Human sig
15	34.4	95.6	1270	12	ADI56382	Adi56382 Human pol
16	34.4	95.6	2022	2	AAQ05731	Aaq05731 Beta 3 ad
17	34.4	95.6	2518	2	AAV23500	Aav23500 Human adr
18	34.4	95.6	2644	8	ABZ42630	Abz42630 Human bet
19	34.4	95.6	2644	11	ADN39372	Adn39372 Cancer/an
20	34.4	95.6	2644	12	ADO29809	Ado29809 Human GPC
21	34.4	95.6	2644	13	ADU50894	Adu50894 Human bet
22	34.4	95.6	2644	14	AEC83014	Aec83014 Breast ca
23	34.4	95.6	2644	14	AEE01346	Aee01346 Human G p
24	34.4	95.6	3682	2	AAQ65476	Aaq65476 Human bet
25	34.4	95.6	5669	13	ADU50893	Adu50893 Human bet
26	32.8	91.1	2000	2	AAQ74367	Aaq74367 Bovine be
27	31.2	86.7	75	10	ADD32084	Add32084 Human bet
28	31.2	86.7	2649	2	AAV30469	Aav30469 Canine be
29	31	86.1	41	6	ABK50104	Abk50104 Sense str
30	30.8	85.6	75	10	ADD32073	Add32073 Human bet
31	30.6	85.0	41	6	ABK50101	Abk50101 Nucleic a
32	29.6	82.2	75	10	ADD32083	Add32083 Human bet
33	29	80.6	34	13	ADT93454	Adt93454 Human bet
34	28	77.8	1203	12	ADO30100	Ado30100 Mouse GPC
35	28	77.8	1920	2	AAQ26808	Aaq26808 Murine ad
36	28	77.8	3437	2	AAQ65477	Aaq65477 Murine be
37	28	77.8	4749	3	AAZ98401	Aaz98401 Sheep bet
38	28	77.8	4749	6	ABK40733	Abk40733 Sheep bet
39	27.4	76.1	34	13	ADT93453	Adt93453 Human bet
40	27.4	76.1	330	2	AAV23501	Aav23501 3T3 deriv
41	27	75.0	27	3	AAA73177	Aaa73177 Beta-3-ad
42	26.4	73.3	1401	12	ADO30098	Ado30098 Mouse GPC
43	26.4	73.3	1525	3	AAZ98405	Aaz98405 Mouse bet
44	26.4	73.3	1525	6	ABK40737	Abk40737 Mouse bet
45	26.4	73.3	4401	3	AAZ98404	Aaz98404 Rhesus mo

ALIGNMENTS

ESULT 1
EC91742/c
D AEC91742 standard; DK; 100 BP.
K
C AEC91742;
K
R 01-DEC-2005 (first entry)
K
E Template B3AR-mt-R(141-240) SEQ ID NO:18.
K
W DNA detection; SNP detection; template; ds.
K
S Synthetic.
K
N JP2005261354-A.
K
D 29-SEP-2005.
K
P 19-MAR-2004; 2004JP-00080974.
K
R 19-MAR-2004; 2004JP-00080974.
V

XX

A (AIST ; KYOTO DAIICHI KAGAKU KK).

XX

PA Inose K;

XX

DR WPI; 2005-662138/68.

XX

PT Detecting target nucleic acid, involves detecting target based on change
PT of fluorescence intensity due to formation or dissociation of hybrid of
PT target nucleic acid and hybridization probe having 5-carboxy fluorescein.

XX

PS Example 6; SEQ ID NO 18; 28pp; Japanese.

XX

CC The invention relates to a method (M1) for detecting a target nucleic
CC acid. (M1) involves measuring the change of fluorescence intensity due to
CC formation or dissociation of the hybrid of the hybridization probe
CC comprising a labeled terminal portion, and a target nucleic acid, and
CC detecting the target nucleic acid based on the change, where the
CC hybridization probe is labeled using the fluorescent pigment chosen from
CC 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
CC -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
CC dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
CC 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
CC hydrazide (Cascade blue). Also described: (1) a real-time PCR method
CC (M2), which involves carrying out real-time PCR using the hybridization
CC probe labeled with the fluorescent pigment, where the hybridization probe
CC is the probe labeled at its terminal with the fluorescent pigment chosen
CC from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
CC curve analysis (M3), which involves using the hybridization probe labeled
CC with the fluorescent pigment, where the hybridization probe is the probe
CC labeled at its terminal with the fluorescent pigment chosen from TAMRA,
CC BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
CC target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
CC target nucleic acid and single nucleotide polymorphisms (SNPs), and in
CC measurement of the ratio of normal type DNA and variant DNA. (M1) enables
CC detection of the nucleic acid by fluorescent detection method, easily and
CC cost effectively. The present sequence represents a template sequence
CC used in an example from the present invention.

XX

SQ Sequence 100 BP; 19 A; 31 C; 34 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 36; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||||||||||||||
Db 76 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 41

RESULT 2
AAX12815
ID AAX12815 standard; DNA; 210 BP.

XX

AC AAX12815;

XX

DT 30-MAR-1999 (first entry)

XX

DE Human biallelic polymorphic DNA fragment ESTD-B3AR.

XX

KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; ss.

XX

OS Homo sapiens.

XX

PN WO9820165-A2.

XX

PD 14-MAY-1998.

XX

PF 05-NOV-1997; 97WO-US020313.

RL 06-NOV-1996; 96US-0030455P.
XX
RA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
RI Lander ES, Wang D, Hudson T;
XX
RL WPI; 1998-286974/25.
XX
PT New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
PS Claim 1; Page 292; 310pp; English.
XX
CC AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 210 BP; 24 A; 71 C; 79 G; 36 T; 0 U; 0 Other;

Query Match 100.0%; Score 36; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||||||||||||||
Db 80 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 115

RESULT 3
ADT93442
ID ADT93442 standard; DNA; 1227 BP.
XX
AC ADT93442;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human beta3 adrenaline receptor (B3AR) C190 variant DNA.
XX
KW single nucleotide polymorphism; SNP; SNP detection;
KW beta3 adrenaline receptor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(190,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX
PN WO2004092385-A1.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-IB005525

R 18-APR-2003; 2003JP-00114381.
X
A (ARKR-) ARKRAY INC.
X
I Hirai M;
X
R WPI; 2004-784610/77.
X
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline
T receptor gene having single nucleotide polymorphism, labeled at terminal
T with fluorescent dye and shows decrease in fluorescence of fluorescent
T dye upon hybridization.
X
S Claim 1; SEQ ID NO 2; 31pp; Japanese.
X
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the human beta3 adrenaline
C receptor (B3AR) C190 variant DNA of the invention.
X
S Sequence 1227 BP; 125 A; 464 C; 391 G; 247 T; 0 U; 0 Other;

Query Match 100.0%; Score 36; DB 13; Length 1227;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
|||||||||||||||||||||||||||||||||||||
D 165 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 200

ESULT 4
AX11762
D AAX11762 standard; DNA; 210 BP.
X
C AAX11762;
X
T 30-MAR-1999 (first entry)
X
E Human biallelic polymorphic DNA fragment ESTD-B3AR.
X
W Polymorphism; biallelic; human; forensic; paternity testing; disease;
W detection; phenotypic typing; characteristic; infection; hereditary;
W autoimmune disease; cancer; inflammation; drug; therapy; medicament;
W treatment; marker; ss.
X
S Homo sapiens.
X
N WO9820165-A2.
X
D 14-MAY-1998.
X
F 05-NOV-1997; 97WO-US020313.
X
R 06-NOV-1996; 96US-0030455P.
X
A (WHED) WHITEHEAD INST BIOMEDICAL RES.
X
I Lander ES, Wang D, Hudson T;
X
R WPI; 1998-286974/25.

DT New isolated nucleic acid segments from the human genome, used for
DT determining polymorphic forms for use in e.g. forensics, paternity
DT testing or phenotypic typing for disease.
XX
SP Claim 1; Page 191; 310pp; English.
XX
CC AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 210 BP; 24 A; 70 C; 79 G; 36 T; 0 U; 1 Other;

 Query Match   100.0%; Score 36; DB 2; Length 210;
 Best Local Similarity   97.2%; Pred. No. 0.0025;
 Matches   35; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Y   1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
             ||||||||||||||||||||||||:||||||||||
C   80 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 115

ESULT 5
EC91757
D   AEC91757 standard; DNA; 420 BP.
XX
C   AEC91757;
XX
DT 01-DEC-2005 (first entry)
XX
DE Template B3AR SEQ ID NO:33.
XX
KW DNA detection; SNP detection; template; ds.
XX
OS Synthetic.
XX
PN JP2005261354-A.
XX
PD 29-SEP-2005.
XX
PF 19-MAR-2004; 2004JP-00080974.
XX
PR 19-MAR-2004; 2004JP-00080974.
XX
PA (KYOT-) KYOTO DAIICHI KAGAKU KK.
XX
IN Inose K;
XX
DR WPI; 2005-662138/68.
XX
DT Detecting target nucleic acid, involves detecting target based on change
DT of fluorescence intensity due to formation or dissociation of hybrid of
DT target nucleic acid and hybridization probe having 5-carboxy fluorescein.
XX
SP Example 10; SEQ ID NO 33; 28pp; Japanese.

The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM), 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto hydrazide (Cascade blue). Also described: (1) a real-time PCR method (M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a template sequence used in an example from the present invention.

Sequence 420 BP; 55 A; 148 C; 142 G; 74 T; 0 U; 1 Other;

Query Match 100.0%; Score 36; DB 14; Length 420;
Best Local Similarity 97.2%; Pred. No. 0.0025;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
             |||||||||||||||||||||||:|||||||||||
D        165 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 200
```

ESULT 6
3K11513
ABK11513 standard; DNA; 2040 BP.

ABK11513;

05-JUN-2002 (first entry)

Human beta-3-adrenergic receptor (ADRB3) gene, generic sequence.

Human; beta-3-adrenergic; receptor; ADRB3; anorectic; ds; antidiabetic;
gene therapy; morbid obesity; insulin resistance;
non-insulin-dependent diabetes mellitus; haplotyping; SNP;
single nucleotide polymorphism.

Homo sapiens.
Synthetic.

WO200208425-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US023223.

21-JUL-2000; 2000US-0220088P.

(GENA-) GENAISSANCE PHARM INC.

Finkel K, Koshy B;

WPI; 2002-241571/29.

Novel genetic variants of beta-3-adrenergic receptor gene useful in studying expression and function of the protein, and for screening drugs

to treat diseases e.g. obesity, non-insulin dependent diabetes mellitus.

XX

SE Example 2; Page 90-91; 91pp; English.

XX

CC The present invention relates to a new polypeptide comprising a sequence
CC which is a polymorphic variant of a reference sequence for ADRB3 (beta-3-
CC adrenergic receptor) protein. The reference sequence comprises a sequence
CC of 408 amino acids as given in the specification, or its fragment, and
CC the polymorphic variant comprises one or more variant amino acids. The
CC polymorphic variants are useful in studying the expression and function
CC of ADRB3, in expressing ADRB3 protein for use in screening for candidate
CC drugs to treat diseases related to ADRB3 activity, in studying the effect
CC of the variation on the biological activity of ADRB3, and the binding
CC affinity of candidate drugs targeting ADRB3 for the treatment of
CC disorders such as morbid obesity, insulin resistance and an early onset
CC of non-insulin-dependent diabetes mellitus. Haplotyping methods are
CC useful in validating ADRB3 as a candidate target for treating a specific
CC condition or disease predicted to be associated with ADRB3 activity, or
CC in the design of clinical trials of candidate drugs for treating a
CC specific condition or disease associated with ADRB3 activity. The present
CC nucleic acid sequence represents the human ADRB3 generic sequence
CC representing all possible single nucleic polymorphisms (SNP) of the gene.
CC This sequence was used in the methods of the invention to facilitate
CC electronic searching of the ADRB3 haplotypes

XX

SQ Sequence 2040 BP; 140 A; 321 C; 351 G; 191 T; 0 U; 1037 Other;

Query Match 100.0%; Score 36; DB 6; Length 2040;
Best Local Similarity 97.2%; Pred. No. 0.0027;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||:||||||||||
Db 485 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 520

RESULT 7
ADZ42281
ID ADZ42281 standard; DNA; 5669 BP.
XX
AC ADZ42281;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human beta-3 adrenoreceptor gene with T1387C SNP Seq 8.
XX
KW renal disease; nephrotropic; SNP detection;
KW single nucleotide polymorphism; SNP; beta-3 adrenoreceptor; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1001. .1197
FT /*tag= a
FT CDS 1198. .3449
FT /*tag= c
FT /product= "Beta-3 adrenoreceptor protein"
FT exon 1198. .2402
FT /*tag= b
FT /number= 1
FT variation 1387
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT intron 2403. .3427
FT /*tag= e
FT /number= 1
FT exon 3428. .3449
FT /*tag= f
FT /number= 2
FT 3'UTR 3450. .4669
FT /*tag= g

N JP2005110606-A.
X
D 28-APR-2005.
X
F 09-OCT-2003; 2003JP-00350959.
X
R 09-OCT-2003; 2003JP-00350959.
X
A (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.
A (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
X
R WPI; 2005-326228/34.
X
T Testing hypertensive renal disease factor, by determining polymorphism in
T genotype of gene relevant to hypertensive renal disease, and estimating
T risk factor for hypertensive renal disease based on determined genotype,
T as index.
X
S Claim 1; SEQ ID NO 8; 440pp; Japanese.
X
C This invention relates to a novel method for testing hypertensive renal
C disease. Specifically, it refers to determining polymorphisms in the
C genotype of a gene relevant to hypertensive renal disease and estimating
C the risk factor for developing the disease accordingly. The present
C invention describes identifying gene polymorphisms in at least one of the
C following genes, namely endothelin converting-enzyme 1, mineralocorticoid
C receptor, urotensin II, superoxide-dismutase 3, thiazide sensitivity NaCl
C symporter, guanosine cyclase-A, hepatocyte growth factor, beta-3
C adrenoreceptor, aldosterone synthetase, endothelium nitrogen monoxide
C synthetase, klotho and a sodium-calcium exchanger. Furthermore, it
C provides primers and probes for determining hypertensive renal disease
C factors, in particular in relation to renal diseases including
C hypertensive early renal disease and hypertensive kidney blood flow
C obstruction. The method enables detection of risk factors, and thus helps
C in preventing or delaying renal disease. This polynucleotide sequence is
C the full length human beta-3 adrenoreceptor gene given in an
C exemplification of the invention.
X
Q Sequence 5669 BP; 1120 A; 1583 C; 1585 G; 1380 T; 0 U; 1 Other;

Query Match 100.0%; Score 36; DB 14; Length 5669;
Best Local Similarity 97.2%; Pred. No. 0.0028;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||:|||||||||||
D 1362 CCTGCTGGTCATCGTGGCCATCGCCYGGACTCCGAG 1397

ESULT 8
BK11451
D ABK11451 standard; DNA; 10306 BP.
X
C ABK11451;
X
T 05-JUN-2002 (first entry)
X
E Human beta-3-adrenergic receptor (ADRB3) gene sequence.
X
K Human; beta-3-adrenergic; receptor; ADRB3; gene; anorectic; antidiabetic;
K gene therapy; morbid obesity; insulin resistance;
K non-insulin-dependent diabetes mellitus; haplotyping; SNP;
K single nucleotide polymorphism; chromosome 8p12-p11_2; ds.
X
S Homo sapiens.
X
H Key Location/Qualifiers
F variation replace(3574,A)
F /*tag= a
F /standard_name= "Single nucleotide polymorphism, PS1"

```
FT   variation       replace(3901,C)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism, PS2"
FT   variation       replace(3903,C)
FT                   /*tag= c
FT                   /standard_name= "Single nucleotide polymorphism, PS3"
FT   CDS             4056. .6307
FT                   /*tag= d
FT                   /product= "Human ADRB3 protein"
FT                   /note= "Specifically claimed in claim 27"
FT   exon            4056. .5260
FT                   /*tag= e
FT                   /number= 1
FT   variation       replace(4109,G)
FT                   /*tag= f
FT                   /standard_name= "Single nucleotide polymorphism, PS4"
FT   variation       replace(4245,C)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism, PS5"
FT   variation       replace(4436,T)
FT                   /*tag= h
FT                   /standard_name= "Single nucleotide polymorphism, PS6"
FT   variation       replace(4567,G)
FT                   /*tag= i
FT                   /standard_name= "Single nucleotide polymorphism, PS7"
FT   variation       replace(4849,T)
FT                   /*tag= j
FT                   /standard_name= "Single nucleotide polymorphism, PS8"
FT   variation       replace(4858,T)
FT                   /*tag= k
FT                   /standard_name= "Single nucleotide polymorphism, PS9"
FT   variation       replace(4887,A)
FT                   /*tag= l
FT                   /standard_name= "Single nucleotide polymorphism, PS10"
FT   variation       replace(5112,T)
FT                   /*tag= m
FT                   /standard_name= "Single nucleotide polymorphism, PS11"
FT   variation       replace(5183,T)
FT                   /*tag= n
FT                   /standard_name= "Single nucleotide polymorphism, PS12"
FT   intron          5261. .6285
FT                   /*tag= o
FT                   /number= 1
FT   variation       replace(5274,T)
FT                   /*tag= p
FT                   /standard_name= "Single nucleotide polymorphism, PS13"
FT   variation       replace(5342,G)
FT                   /*tag= q
FT                   /standard_name= "Single nucleotide polymorphism, PS14"
FT   exon            6286. .6307
FT                   /*tag= r
FT                   /number= 2
FT   variation       replace(6349,A)
FT                   /*tag= s
FT                   /standard_name= "Single nucleotide polymorphism, PS15"
FT   variation       replace(6557,C)
FT                   /*tag= t
FT                   /standard_name= "Single nucleotide polymorphism, PS16"
FT   variation       replace(6561,T)
FT                   /*tag= u
FT                   /standard_name= "Single nucleotide polymorphism, PS17"
XX
PN   WO200208425-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-US023223.
XX
PR   21-JUL-2000; 2000US-0220088P.
XX
PA   (GENA ) GENAISSANCE PHARM INC.
```

!--StartFragment-->
ESULT 1
3-08-087-772A-14
Sequence 14, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1134 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
M◎LECULE TYPE: DNA (genomic)
3-08-087-772A-14

Query Match 95.6%; Score 34.4; DB 2; Length 1134;
Best Local Similarity 97.2%; Pred. No. 0.0021;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||| |||||||||
o 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

ESULT 2
3-09-993-844A-13
Sequence 13, Application US/09993844A
Patent No. 7018812
GENERAL INFORMATION:
APPLICANT: Oakley, Robert H.
APPLICANT: Barak, Lawrence S.
APPLICANT: Laporte, Stephane A.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Modified G-Protein Coupled Receptors
FILE REFERENCE: 033072-026
CURRENT APPLICATION NUMBER: US/09/993,844A
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/260,363
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 82

SEQ ID NO 13
LENGTH: 1185
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotide sequence of beta3-AR-V2R chimera
3-09-993-844A-13

Query Match 95.6%; Score 34.4; DB 5; Length 1185;
Best Local Similarity 97.2%; Pred. No. 0.0021;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||| |||||||||
D 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

RESULT 3
3-07-916-901-1
Sequence 1, Application US/07916901
Patent No. 5364772
GENERAL INFORMATION:
APPLICANT: Granneman, James G.
APPLICANT: Lahners, Kristine N.
APPLICANT: Rao, Donald D.
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
ADDRESSEE: MILTON
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: USA
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,901
FILING DATE: 19920720
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324(WSU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1224
3-07-916-901-1

Query Match 95.6%; Score 34.4; DB 2; Length 1227;
Best Local Similarity 97.2%; Pred. No. 0.0021;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||| |||||||||
D 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

ESULT 4
3-08-351-473B-7
Sequence 7, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-351-473B-7

Query Match 95.6%; Score 34.4; DB 2; Length 1227;
Best Local Similarity 97.2%; Pred. No. 0.0021;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||||| |||||||||
D 165 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 200

ESULT 5
3-09-016-434-1184
Sequence 1184, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3171 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1184:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g178895
3-09-016-434-1184

Query Match 95.6%; Score 34.4; DB 3; Length 1270;
Best Local Similarity 97.2%; Pred. No. 0.0021;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||| ||||||||||
o 202 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 237

ESULT 6
3-08-450-962-1
Sequence 1, Application US/08450962
Patent No. 6274706
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROSBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
CLASSIFICATION: 530

APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3683 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
3-08-450-962-1

Query Match 95.6%; Score 34.4; DB 3; Length 3683;
Best Local Similarity 97.2%; Pred. No. 0.0022;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAG 36
||||||||||||||||||||||||| ||||||||||
o 802 CCTGCTGGTCATCGTGGCCATCGCCTGGACTCCGAG 837

ESULT 7
!--EndFragment-->

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104107_us-10-553-509-10.szlm60.rnpbm.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104107_us-10-53-509-10.szlm60.rnpbm.

tart

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 06:59:56 ; Search time 717.371 Seconds
(without alignments)
308.317 Million cell updates/sec

itle: US-10-553-509-10
erfect score: 18
equence: 1 catcgcctggactccgag 18

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 18892170 seqs, 6143817638 residues

otal number of hits satisfying chosen parameters: 24217294

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description

	1	18	100.0	41	8	US-10-398-445-7	Sequence 7, Appli
	2	18	100.0	41	8	US-10-398-445-7	Sequence 7, Appli
	3	17.6	100.0	21	10	US-10-831-997-1650	Sequence 1650, Ap
	4	17.6	100.0	29	7	US-10-336-638-896	Sequence 896, App
	5	17.6	100.0	41	8	US-10-398-445-1	Sequence 1, Appli
	6	17.6	100.0	42	10	US-10-730-771-38	Sequence 38, Appl
	7	17	94.4	19	8	US-10-398-445-2	Sequence 2, Appli
	8	16.4	91.1	22	3	US-09-257-650-3	Sequence 3, Appli
	9	16.4	91.1	26	3	US-09-576-715A-8	Sequence 8, Appli
	10	16.4	91.1	41	8	US-10-398-445-4	Sequence 4, Appli
	11	16.4	91.1	41	8	US-10-398-445-6	Sequence 6, Appli
	12	15.6	86.7	21	10	US-10-831-997-1651	Sequence 1651, Ap
	13	15	83.3	25	8	US-10-719-956-681619	Sequence 681619,
	14	14.8	82.2	25	11	US-10-933-982-178318	Sequence 178318,
	15	14.8	82.2	25	13	US-11-036-317-482682	Sequence 482682,
	16	14.4	80.0	25	6	US-10-098-263B-43003	Sequence 43003, A
	17	14.4	80.0	25	6	US-10-098-263B-43631	Sequence 43631, A
	18	14.4	80.0	25	15	US-11-121-849-250204	Sequence 250204,
	19	14	77.8	25	9	US-10-719-900-374208	Sequence 374208,
	20	13.8	76.7	19	14	US-11-083-784-1210384	Sequence 1210384,
	21	13.8	76.7	19	15	US-11-101-244-1210384	Sequence 1210384,
	22	13.8	76.7	25	6	US-10-098-263B-104983	Sequence 104983,
	23	13.6	75.6	34	13	US-11-003-839-11	Sequence 11, Appl
	24	13.6	75.6	34	16	US-11-230-462-11	Sequence 11, Appl
	25	13.6	75.6	41	8	US-10-035-833A-3782	Sequence 3782, Ap
	26	13.6	75.6	41	8	US-10-035-833A-3783	Sequence 3783, Ap
	27	13.4	74.4	19	14	US-11-083-784-195789	Sequence 195789,
	28	13.4	74.4	19	14	US-11-083-784-195891	Sequence 195891,
	29	13.4	74.4	19	14	US-11-083-784-195989	Sequence 195989,
	30	13.4	74.4	19	15	US-11-101-244-195789	Sequence 195789,
	31	13.4	74.4	19	15	US-11-101-244-195891	Sequence 195891,
	32	13.4	74.4	19	15	US-11-101-244-195989	Sequence 195989,
	33	13.4	74.4	19	15	US-11-069-908-2272	Sequence 2272, Ap
	34	13.4	74.4	19	15	US-11-069-908-4638	Sequence 4638, Ap
	35	13.4	74.4	23	11	US-10-310-914A-940181	Sequence 940181,
	36	13.4	74.4	25	8	US-10-719-956-59998	Sequence 59998, A
	37	13.4	74.4	25	8	US-10-719-956-110194	Sequence 110194,
	38	13.4	74.4	25	8	US-10-719-956-115498	Sequence 115498,
	39	13.4	74.4	25	8	US-10-719-956-305844	Sequence 305844,
	40	13.4	74.4	25	8	US-10-719-956-681620	Sequence 681620,
	41	13.4	74.4	25	9	US-10-719-900-248512	Sequence 248512,
	42	13.4	74.4	26	10	US-10-708-204-5426	Sequence 5426, Ap
	43	13.4	74.4	27	10	US-10-708-204-5416	Sequence 5416, Ap
	44	13.4	74.4	35	3	US-09-423-800-21	Sequence 21, Appl
	45	13.4	74.4	35	6	US-10-182-018-21	Sequence 21, Appl

ALIGNMENTS

ESULT 1
3-10-398-445-5
Sequence 5, Application US/10398445
Publication No. US20040166498A1
GENERAL INFORMATION:
APPLICANT: PETERSON, RAYMOND J.
TITLE OF INVENTION: COMPUTER SYSTEM FOR DESIGNING OLIGONUCLEOTIDES USED IN
TITLE OF INVENTION: BIOCHEMICAL METHODS
FILE REFERENCE: 35804-188435
CURRENT APPLICATION NUMBER: US/10/398,445
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: PCT/US01/31037
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/237,383
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
3-10-398-445-5

Query Match 100.0%; Score 18; DB 8; Length 41;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
o 14 CATCGCCTGGACTCCGAG 31

ESULT 2
3-10-398-445-7/c
Sequence 7, Application US/10398445
Publication No. US20040166498A1
GENERAL INFORMATION:
APPLICANT: PETERSON, RAYMOND J.
TITLE OF INVENTION: COMPUTER SYSTEM FOR DESIGNING OLIGONUCLEOTIDES USED IN
TITLE OF INVENTION: BIOCHEMICAL METHODS
FILE REFERENCE: 35804-188435
CURRENT APPLICATION NUMBER: US/10/398,445
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: PCT/US01/31037
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/237,383
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 7
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
3-10-398-445-7

Query Match 100.0%; Score 18; DB 8; Length 41;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
o 28 CATCGCCTGGACTCCGAG 11

ESULT 3
3-10-831-997-1650
Sequence 1650, Application US/10831997
Publication No. US20050244834A1
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/10/831,997
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: US/09/657,472
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724

NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1650
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
3-10-831-997-1650

Query Match 100.0%; Score 18; DB 10; Length 21;
Best Local Similarity 94.4%; Pred. No. 38;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
y          1 CATCGCCTGGACTCCGAG 18
             ||||||:||||||||||
o          4 CATCGCCYGGACTCCGAG 21
```

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104100_us-10-553-509-10.szlm60.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104100_us-10-53-509-10.szlm60.rng.

tart | next page

Go Back to previous pag

```
                        GenCore version 5.1.9
                  Copyright (c) 1993 - 2006  Biocceleration Ltd.


M nucleic - nucleic search, using sw model

un on:          December 15, 2006, 05:57:43 ; Search time 217.011 Seconds
                                            (without alignments)
                                           578.313 Million cell updates/sec

itle:           US-10-553-509-10
erfect score:   18
equence:        1 catcgcctggactccgag 18

coring table:   IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

earched:        5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters:      5397982

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

atabase :        N_Geneseq_8:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

                 %
esult            Query
  No.    Score  Match Length DB  ID                          Description
---------------------------------------------------------------------------
```

3	18	100.0	21	4	AAF96885	Aaf96885 Human gen
4	18	100.0	25	12	ADO26525	Ado26525 Novel hyb
5	18	100.0	26	6	ABL40567	Abl40567 Primer #7
6	18	100.0	34	13	ADT93453	Adt93453 Human bet
7	17.6	100.0	21	3	AAC73164	Aac73164 SNP flank
8	17.6	100.0	29	3	AAA04696	Aaa04696 Polymorph
9	17.6	100.0	41	6	ABK50101	Abk50101 Nucleic a
10	17	94.4	17	2	AAT58989	Aat58989 Obesity a
11	17	94.4	17	2	AAT58987	Aat58987 Obesity a
12	17	94.4	17	14	AEC91758	Aec91758 Probe 5T-
13	17	94.4	18	14	AEC91756	Aec91756 Probe 3T-
14	17	94.4	19	6	ABK50102	Abk50102 Allele sp
15	16.4	91.1	19	13	ADT93446	Adt93446 Fluoresce
16	16.4	91.1	25	6	ABL40568	Abl40568 Primer #8
17	16.4	91.1	25	12	ADO26526	Ado26526 Novel hyb
18	16.4	91.1	34	13	ADT93454	Adt93454 Human bet
19	16.4	91.1	41	6	ABK50104	Abk50104 Sense str
20	16	88.9	16	13	ADT93451	Adt93451 Fluoresce
21	16	88.9	21	4	AAF96886	Aaf96886 Human gen
22	15.4	85.6	17	2	AAT58988	Aat58988 Obesity a
23	15.4	85.6	17	2	AAT58990	Aat58990 Obesity a
24	15.4	85.6	21	14	AEC91760	Aec91760 Probe 3T-
25	15.4	85.6	51	4	AAH90342	Aah90342 Human clo
26	15.4	85.6	51	4	AAH90341	Aah90341 Human clo
27	15	83.3	15	13	ADT93452	Adt93452 Fluoresce
28	14.4	80.0	25	9	ACI43012	Aci43012 Human mic
29	14.4	80.0	25	9	ACI43640	Aci43640 Human mic
30	14	77.8	14	13	ADU50896	Adu50896 Human bet
31	14	77.8	14	14	ADZ42342	Adz42342 FAM probe
32	14	77.8	41	6	ABZ46998	Abz46998 Human ATP
33	14	77.8	41	6	ABZ46999	Abz46999 Human ATP
34	13.8	76.7	25	9	ACK05002	Ack05002 Human mic
35	13.6	75.6	34	2	AAV33317	Aav33317 Anti-CD23
36	13.4	74.4	16	13	ADT93445	Adt93445 Fluoresce
37	13.4	74.4	19	14	AEC28618	Aec28618 Human all
38	13.4	74.4	19	14	AEC26252	Aec26252 Human all
39	13.4	74.4	25	4	AAC89164	Aac89164 Sample DN
40	13.4	74.4	33	2	AAQ87254	Aaq87254 Primer fo
41	13.4	74.4	35	2	AAV24264	Aav24264 Chimeric
42	13.4	74.4	35	2	AAX00108	Aax00108 Human ant
43	13.4	74.4	35	3	AAZ58889	Aaz58889 PCR prime
44	13.4	74.4	35	4	AAF69217	Aaf69217 Chimeric
45	13.4	74.4	35	4	AAF69105	Aaf69105 Chimeric

ALIGNMENTS

```
ESULT 1
DT93450
D   ADT93450 standard; DNA; 18 BP.
K
C   ADT93450;
K
R   13-JAN-2005  (first entry)
K
E   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.
K
W   SNP detection; beta3 adrenaline receptor; ss; probe.
K
S   Homo sapiens.
K
H   Key             Location/Qualifiers
F   modified_base   1
F                   /*tag=  a
F                   /mod_base= OTHER
F                   /note= "OTHER = Linked to BODIPY FL group"
F   modified_base   18
F                   /*tag=  b
F                   /mod_base= OTHER
```

XX
XX WO2004092385-A1.
XX
XX 28-OCT-2004.
XX
XX 16-APR-2004; 2004WO-JP005525.
XX
XX 18-APR-2003; 2003JP-00114381.
XX
XX (ARKR-) ARKRAY INC.
XX
XX Hirai M;
XX
XX WPI; 2004-784610/77.
XX
XX Nucleic acid probe useful for detecting mutation in beta3 adrenaline
XX receptor gene having single nucleotide polymorphism, labeled at terminal
XX with fluorescent dye and shows decrease in fluorescence of fluorescent
XX dye upon hybridization.
XX
XX Claim 2; SEQ ID NO 10; 31pp; Japanese.
XX
XX The invention relates to a novel nucleic acid probe which is labelled at
XX a terminal with a fluorescent dye, whereby a decrease in the fluorescence
XX of the fluorescent dye is observed upon hybridisation. The probe
XX comprises a base sequence derived from a fully defined sequence of 1227
XX nucleotides as given in the specification and being labelled at the 3' or
XX 5' end with a fluorescent dye. The probe of the invention may be useful
XX for detecting a mutation or single nucleotide polymorphism (SNP) in the
XX beta3 adrenaline receptor (B3AR) gene. The probe is effective in
XX detecting a B3AR Trp64Arg mutation within a short time whilst risk of
XX contamination of the amplified product is prevented and the process is
XX automated. The current sequence is that of the fluorescent-labelled probe
XX (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
XX receptor (B3AR) T190 variant DNA.
XX
XX Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
Db 1 CATCGCCTGGACTCCGAG 18

RESULT 2
ADT93449
ID ADT93449 standard; DNA; 20 BP.
XX
AC ADT93449;
XX
DT 13-JAN-2005 (first entry)
XX
DE Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.
XX
KW SNP detection; beta3 adrenaline receptor; ss; probe.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Linked to BODIPY FL group"
FT modified_base 20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER = Linked to R group"

N WO2004092385-A1.
XX
D 28-OCT-2004.
XX
F 16-APR-2004; 2004WO-JP005525.
XX
R 18-APR-2003; 2003JP-00114381.
XX
PA (ARKR-) ARKRAY INC.
XX
PI Hirai M;
XX
DR WPI; 2004-784610/77.
XX
PT Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT receptor gene having single nucleotide polymorphism, labeled at terminal
PT with fluorescent dye and shows decrease in fluorescence of fluorescent
PT dye upon hybridization.
XX
PS Claim 2; SEQ ID NO 9; 31pp; Japanese.
XX
CC The invention relates to a novel nucleic acid probe which is labelled at
CC a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC of the fluorescent dye is observed upon hybridisation. The probe
CC comprises a base sequence derived from a fully defined sequence of 1227
CC nucleotides as given in the specification and being labelled at the 3' or
CC 5' end with a fluorescent dye. The probe of the invention may be useful
CC for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC contamination of the amplified product is prevented and the process is
CC automated. The current sequence is that of the fluorescent-labelled probe
CC (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC receptor (B3AR) T190 variant DNA.
XX
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAG 18
     ||||||||||||||||||
D 1 CATCGCCTGGACTCCGAG 18

ESULT 3
AF96885
ID AAF96885 standard; DNA; 21 BP.
XX
AC AAF96885;
XX
DT 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1646.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT variation 11
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"

XX

DT 15-MAR-2001.

XX

PR 07-SEP-2000; 2000WO-US024503.

XX

PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.

WO200118250 # 21

XX

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.

XX

PI [redacted] Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;

XX

DR WPI; 2001-226749/23.

XX

PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.

XX

PS Example; Page 159; 242pp; English.

XX

CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPS shown in the specification
CC
CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a captial V

XX

SQ Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
Db 4 CATCGCCTGGACTCCGAG 21

RESULT 4
AD026525
ID ADO26525 standard; DNA; 25 BP.

XX

AC ADO26525;

XX

DT 12-AUG-2004 (first entry)

XX

DE Novel hybridisation detection-related oligonucleotide SeqID1.

XX

KW hybridisation detection; immobilised probe; AC impedance;
KW foetal genome analysis; ss.

XX

OS Unidentified.

XX

PN WO2004044570-A1.

XX

PD 27-MAY-2004.

XX

PF 30-SEP-2003; 2003WO-JP012499.

XX

XX
PA (TOYA-) TOYAMA PREFECTURE.
PA (COSE-) COSEL CO LTD.
PA (TATE-) TATEYAMA KAGAKU IND CO LTD.
PA (TOXX) TOYO KAKO CO LTD.
XX
IN Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
IN Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
XX
PR WPI; 2004-420427/39.
XX
TI Detection of hybridization of an immobilized probe to a target nucleic
TI acid by measuring AC impedance across the carrier surface for specific
TI gene detection in investigation and diagnosis of disease.
XX
PS Example; SEQ ID NO 1; 33pp; Japanese.
XX
CC This invention relates to a novel method of detecting hybridisation of an
CC immobilised probe to a target nucleic acid using measurement of AC
CC impedance. Detection of specific genes and gene sequences in nucleic acid
CC samples (such as samples of genomic DNA) may be useful for diagnosis,
CC prediction and prevention of genetic disorders and analysis of foetal
CC genome. Hybridisation is detected with high accuracy and sensitivity
CC without the use of dyes. The present sequence is that of an
CC oligonucleotide which was used in the exemplification of the invention.
XX
SQ Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
Db 6 CATCGCCTGGACTCCGAG 23

RESULT 5
ABL40567
ID ABL40567 standard; DNA; 26 BP.
XX
AC ABL40567;
XX
DT 17-JUN-2002 (first entry)
XX
DE Primer #7 used in a base polymorphism detection method.
XX
KW Polymorphism; nucleic acid detection; endonuclease; probe; ADRB2;
KW hybridisation; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP2002034598-A.
XX
PD 05-FEB-2002.
XX
PF 27-JUL-2000; 2000JP-00226912.
XX
PR 27-JUL-2000; 2000JP-00226912.
XX
PA (TOYM) TOYOBO KK.
XX
PR WPI; 2002-298820/34.
XX
DT Detection of base polymorphism.
XX
PS Disclosure; Page 10; 10pp; Japanese.
XX
CC The invention relates to a method for detecting base polymorphism. The
CC method involves (1) amplifying the nucleic acid fragment containing base

polymorphism of the specific nucleic acid sequence; (2) hybridizing the amplified nucleic acid with at least two polymorphism-specific probes; (3) treating with RNA-selective cleavage endonuclease; (4) measuring detecting signals of each probe; and (5) identifying polymorphism by the ratio of each detecting signals. The probe can be used for detecting base polymorphism. The present sequence represents a PCR primer used in the course of the invention

Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCCGAG 18
             ||||||||||||||||||
D          9 CATCGCCTGGACTCCGAG 26
```

ESULT 6
DT93453
D ADT93453 standard; DNA; 34 BP.
K
C ADT93453;
K
I 13-JAN-2005 (first entry)
K
E Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.
K
W single nucleotide polymorphism; SNP; SNP detection;
W beta3 adrenaline receptor; ds.
K
S Homo sapiens.
K
H Key Location/Qualifiers
I variation replace(19,C)
I /*tag= a
I /standard_name= "Single nucleotide polymorphism"
K
N WO2004092385-A1.
K
D 28-OCT-2004.
K
F 16-APR-2004; 2004WO-JP005525.
K
R 18-APR-2003; 2003JP-00114381.
K
A (ARKR-) ARKRAY INC.
K
I Hirai M;
K
R WPI; 2004-784610/77.
K
I Nucleic acid probe useful for detecting mutation in beta3 adrenaline
I receptor gene having single nucleotide polymorphism, labeled at terminal
I with fluorescent dye and shows decrease in fluorescence of fluorescent
I dye upon hybridization.
K
S Example 1; Fig 1; 31pp; Japanese.
K
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the human beta3 adrenaline

receptor (BSAR) 1190 variant DNA fragment of the invention.
XX
SQ Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
Db 12 CATCGCCTGGACTCCGAG 29

RESULT 7
AAC73164
ID AAC73164 standard; DNA; 21 BP.
XX
AC AAC73164;
XX
DT 02-FEB-2001 (first entry)
XX
DE SNP flanking sequence #24 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
PS Example 7; Page 50; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one such polymorphic locus
CC used in the present invention. The amplified nucleic acid product is then
CC used as a template in a SBE reaction with an extension primer. The SBE
CC reaction products are used to form the oligonucleotide array. Note: This
CC sequence includes a SNP represented by the degenerate codon in the
CC sequence
XX
SQ Sequence 21 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 1 Other;

Query Match 100.0%; Score 18; DB 3; Length 21;
Best Local Similarity 94.4%; Pred. No. 51;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCCGAG 18
|||||||.||||||||||

ESULT 8
AA04696
D AAA04696 standard; DNA; 29 BP.
K
C AAA04696;
K
I 22-MAY-2000 (first entry)
K
E Polymorphic fragment of hypertension associated gene ADRB3.
K
W Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
W Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
W Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
W polycystic kidney disease; von Willebrands disease; forensic; human;
W tuberous sclerosis; hereditary hemorrhagica telangiectasia;
W familial colonic polyposis; osteogenesis imperfecta; porphyria;
W Ehlers-Danlos syndrome; ss.
K
S Homo sapiens.
K
N EP955382-A2.
K
D 10-NOV-1999.
K
F 07-MAY-1999; 99EP-00250150.
K
R 07-MAY-1998; 98US-0084641P.
R 03-MAY-1999; 99US-00304232.
K
A (AFFY-) AFFYMETRIX INC.
A (UYCA-) UNIV CASE WESTERN RESERVE.
K
I Fan JB, Chakravarti A, Haluska MK;
K
R WPI; 2000-107928/10.
K
T Novel nucleic acids containing polymorphisms used in the diagnosis of
T hypertension.
K
S Disclosure; Page 45; 53pp; English.
K
C The invention provides polymorphic fragments of genes associated with
C hypertension. The nucleic acids including the polymorphic sites can be
C used as probes or primers for expressing variant proteins. Detection of
C the polymorphisms is useful in designing prophylactic and therapeutic
C regimes customized to underlying abnormalities. The polymorphisms can be
C used for association studies for hypertension, and in hypertension
C diagnostic assays. Where the polymorphisms have strong correlation with
C hypertension, within a gene, they are likely to have a causative role in
C hypertension. This information can be used to find the precise role of a
C polymorphism in the disease, and this can be used to identify potential
C drugs which combat the disease. The polymorphisms can be tested for
C association with other diseases e.g. agammaglobulinemia, diabetes
C insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
C syndrome, Fabrys disease, familial hypercholesterolemia, polycystic
C kidney disease, hereditary spherocytosis, von Willebrands disease,
C tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
C colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
C acute intermittent porphyria. The polymorphic forms can also be used in
C forensics to identify individuals
K
Q Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 18; DB 3; Length 29;
Best Local Similarity 94.4%; Pred. No. 51;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
                  ||||||||:|||||||||||
Db          8 CATCGCCYGGACTCCGAG 25


ESULT 9
3K50101
D   ABK50101 standard; DNA; 41 BP.
K
C   ABK50101;
K
T   15-JUL-2002  (first entry)
K
E   Nucleic acid sequence used for sequence formatting.
K
W   Optimal reagent oligonucleotide; target nucleic acid evaluation;
W   target feature; exclusion value; ranking value; sequence window;
W   sequence formatting; ds.
K
S   Synthetic.
K
N   WO200229379-A2.
K
D   11-APR-2002.
K
F   04-OCT-2001; 2001WO-US031037.
K
R   04-OCT-2000; 2000US-0237383P.
K
A   (CELA-) CELADON LAB INC.
K
I   Peterson RJ;
K
R   WPI; 2002-340129/37.
K
T   Determining an optimal reagent oligonucleotide for evaluating a target
T   nucleic acid having a target feature, involves defining a set of
T   exclusion values and/or ranking values specific to a biochemical method.
K
S   Example; Fig 1B; 91pp; English.
K
C   The present invention relates to a new method for determining an optimal
C   reagent oligonucleotide for evaluating a target nucleic acid having a
C   target feature. The method comprises defining a set of exclusion values
C   and/or ranking values specific to the method, defining a sequence window
C   adjacent to the target, and generating candidate reagent oligonucleotides
C   complementary to the sense and/or antisense strands of the target within
C   the window. The method can be used for determining an optimal reagent
C   oligonucleotide sequence for use in a biochemical method for evaluating a
C   target nucleic acid sequence having a target feature. The present nucleic
C   acid sequence represent a DNA molecule used in the methods of the
C   invention for nucleic acid sequence formatting
K
Q   Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

 Query Match             100.0%;  Score 18;  DB 6;  Length 41;
 Best Local Similarity   94.4%;  Pred. No. 52;
 Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 CATCGCCTGGACTCCGAG 18
                 |||||||:||||||||||
Db          14 CATCGCCYGGACTCCGAG 31


ESULT 10
AT58989
D   AAT58989 standard; DNA; 17 BP.
K
C   AAT58989;
K
T   04-AUG-1997 . (first entry)
```

XX
KW   Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;
KW   beta3AR; ss.
XX
OS   Synthetic.
XX
PN   WO9636641-A1.
XX
PD   21-NOV-1996.
XX
PF   17-MAY-1996;   96WO-US007218.
XX
PR   19-MAY-1995;   95US-00446530.
XX
PA   (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI   Shuldiner AR, Walston J, Silver K, Roth J;
XX
DR   WPI; 1997-012034/01.
XX
DT   New isolated beta3-adrenergic receptor mutation - used to develop prods.
DT   for the diagnosis and treatment of type II diabetes and/or obesity.
XX
CC   Claim 17; Page 42; 51pp; English.
XX
CC   The present sequence is a nucleic acid probe used in a method for
CC   diagnosis of a subject having or at risk of having type II diabetes
CC   mellitus and/or obesity. The method involves contacting a target nucleic
CC   acid of a sample from the subject with a nucleic acid probe (preferably
CC   the present sequence or that in AAT58990) that detects a mutation in the
CC   beta3-adrenergic receptor (beta3AR) gene. The present sequence can also
CC   be used in the treatment of subjects having or at risk of having type II
CC   diabetes and/or obesity
XX
SQ   Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

 Query Match   94.4%; Score 17; DB 2; Length 17;
 Best Local Similarity   100.0%; Pred. No. 1e+02;
 Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCGA 17
              |||||||||||||||||
Db   1 CATCGCCTGGACTCCGA 17

RESULT 11
AAT58987/c
ID   AAT58987 standard; DNA; 17 BP.
XX
AC   AAT58987;
XX
DT   04-AUG-1997 (first entry)
XX
DE   Obesity and type II diabetes mellitus diagnosis target nucleic acid.
XX
KW   Hybridisation; polymerase chain reaction; beta3-adrenergic receptor;
KW   beta3AR; ss.
XX
OS   Synthetic.
XX
PN   WO9636641-A1.
XX
PD   21-NOV-1996.
XX
PF   17-MAY-1996;   96WO-US007218.
XX
PR   19-MAY-1995;   95US-00446530.
XX
PA   (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.

XX
RX   .WPI; 1997-012034/01.
XX
PT   New isolated beta3-adrenergic receptor mutation - used to develop prods.
PT   for the diagnosis and treatment of type II diabetes and/or obesity.
XX
PS   Claim 16; Page 42; 51pp; English.
XX
CC   The present sequence is a target nucleic acid detected in a method for
CC   diagnosis of a subject having or at risk of having type II diabetes
CC   mellitus and/or obesity. The method involves contacting a target nucleic
CC   acid of a sample from the subject (preferably the present sequence or
CC   that in AAT58988) with a nucleic acid probe that detects a mutation in
CC   the beta3-adrenergic receptor (beta3AR) gene
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

 Query Match   94.4%; Score 17; DB 2; Length 17;
 Best Local Similarity   100.0%; Pred. No. 1e+02;
 Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCGA 17
              |||||||||||||||||
Db   17 CATCGCCTGGACTCCGA 1

RESULT 12
AEC91758/c
ID   AEC91758 standard; DNA; 17 BP.
XX
AC   AEC91758;
XX
DT   01-DEC-2005 (first entry)
XX
DE   Probe 5T-B3AR-w-IMS-R2-17 SEQ ID NO:34.
XX
KW   DNA detection; SNP detection; probe; ss.
XX
OS   Synthetic.
XX
PN   JP2005261354-A.
XX
PD   29-SEP-2005.
XX
PF   19-MAR-2004; 2004JP-00080974.
XX
PR   19-MAR-2004; 2004JP-00080974.
XX
PA   (KYOT-) KYOTO DAIICHI KAGAKU KK.
XX
PI   Inose K;
XX
DR   WPI; 2005-662138/68.
XX
PT   Detecting target nucleic acid, involves detecting target based on change
PT   of fluorescence intensity due to formation or dissociation of hybrid of
PT   target nucleic acid and hybridization probe having 5-carboxy fluorescein.
XX
PS   Example 10; SEQ ID NO 34; 28pp; Japanese.
XX
CC   The invention relates to a method (M1) for detecting a target nucleic
CC   acid. (M1) involves measuring the change of fluorescence intensity due to
CC   formation or dissociation of the hybrid of the hybridization probe
CC   comprising a labeled terminal portion, and a target nucleic acid, and
CC   detecting the target nucleic acid based on the change, where the
CC   hybridization probe is labeled using the fluorescent pigment chosen from
CC   6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
CC   -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
CC   dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
CC   5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo-1-pyrenyl)oxy]acete

(M2), which involves carrying out real-time PCR using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-curve analysis (M3), which involves using the hybridization probe labeled with the fluorescent pigment, where the hybridization probe is the probe labeled at its terminal with the fluorescent pigment chosen from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a target nucleic acid. (M1)-(M3) are useful for detecting mutations in a target nucleic acid and single nucleotide polymorphisms (SNPs), and in measurement of the ratio of normal type DNA and variant DNA. (M1) enables detection of the nucleic acid by fluorescent detection method, easily and cost effectively. The present sequence represents a probe used in an example from the present invention.

Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 CATCGCCTGGACTCCGA 17
             |||||||||||||||||
o         17 CATCGCCTGGACTCCGA 1
```

ESULT 13
EC91756/c
AEC91756 standard; DNA; 18 BP.

AEC91756;

01-DEC-2005 (first entry)

Probe 3T-B3AR-w-IMS-R1-18 SEQ ID NO:32.

DNA detection; SNP detection; probe; ss.

Synthetic.

JP2005261354-A.

29-SEP-2005.

19-MAR-2004; 2004JP-00080974.

19-MAR-2004; 2004JP-00080974.

(KYOT-) KYOTO DAIICHI KAGAKU KK.

Inose K;

WPI; 2005-662138/68.

Detecting target nucleic acid, involves detecting target based on change of fluorescence intensity due to formation or dissociation of hybrid of target nucleic acid and hybridization probe having 5-carboxy fluorescein.

Example 10; SEQ ID NO 32; 28pp; Japanese.

The invention relates to a method (M1) for detecting a target nucleic acid. (M1) involves measuring the change of fluorescence intensity due to formation or dissociation of the hybrid of the hybridization probe comprising a labeled terminal portion, and a target nucleic acid, and detecting the target nucleic acid based on the change, where the hybridization probe is labeled using the fluorescent pigment chosen from 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),

C hybridise (cascade blue). Also described: (1) a real-time PCR method
C (M2), which involves carrying out real-time PCR using the hybridization
C probe labeled with the fluorescent pigment, where the hybridization probe
C is the probe labeled at its terminal with the fluorescent pigment chosen
C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
C curve analysis (M3), which involves using the hybridization probe labeled
C with the fluorescent pigment, where the hybridization probe is the probe
C labeled at its terminal with the fluorescent pigment chosen from TAMRA,
C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
C target nucleic acid and single nucleotide polymorphisms (SNPs), and in
C measurement of the ratio of normal type DNA and variant DNA. (M1) enables
C detection of the nucleic acid by fluorescent detection method, easily and
C cost effectively. The present sequence represents a probe used in an
C example from the present invention.
XX
SQ Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

 Query Match   94.4%; Score 17; DB 14; Length 18;
 Best Local Similarity   100.0%; Pred. No. 1e+02;
 Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   2 ATCGCCTGGACTCCGAG 18
            |||||||||||||||||
D   18 ATCGCCTGGACTCCGAG 2

ESULT 14
ABK50102
ID ABK50102 standard; DNA; 19 BP.
XX
AC ABK50102;
XX
DT 15-JUL-2002 (first entry)
XX
DE Allele specific hybridisation probe.
XX
KW Optimal reagent oligonucleotide; target nucleic acid evaluation;
KW target feature; exclusion value; ranking value; sequence window;
KW hybridisation; probe; ss.
XX
OS Synthetic.
XX
PN WO200229379-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031037.
XX
PR 04-OCT-2000; 2000US-0237383P.
XX
PA (CELA-) CELADON LAB INC.
XX
PI Peterson RJ;
XX
DR WPI; 2002-340129/37.
XX
PT Determining an optimal reagent oligonucleotide for evaluating a target
PT nucleic acid having a target feature, involves defining a set of
PT exclusion values and/or ranking values specific to a biochemical method.
XX
PS Example; Fig 2A; 91pp; English.
XX
CC The present invention relates to a new method for determining an optimal
CC reagent oligonucleotide for evaluating a target nucleic acid having a
CC target feature. The method comprises defining a set of exclusion values
CC and/or ranking values specific to the method, defining a sequence window
CC adjacent to the target, and generating candidate reagent oligonucleotides
CC complementary to the sense and/or antisense strands of the target within
CC the window. The method can be used for determining an optimal reagent
C oligonucleotide sequence for use in a biochemical method for evaluating a

C acid sequence represent an allele specific hybridisation probe that was
C used in the methods of the invention in numbering systems
K
Q Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGA 17
     |||||||||||||||||
D 3 CATCGCCTGGACTCCGA 19

ESULT 15
DT93446
D ADT93446 standard; DNA; 19 BP.
K
C ADT93446;
K

```
!--StartFragment-->RESULT 1
D107586
OCUS       BD107586                 26 bp    DNA     linear   PAT 18-SEP-2002
EFINITION  Method for detecting base polymorphism.
CCESSION   BD107586
ERSION     BD107586.1  GI:23202404
EYWORDS    JP 2002034598-A/7.
OURCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1  (bases 1 to 26)
 AUTHORS   Yoshiga,S., Takarada,Y., Aono,T. and Segawa,M.
 TITLE     Method for detecting base polymorphism
 JOURNAL   Patent: JP 2002034598-A 7 05-FEB-2002;
           TOYOBO CO LTD
OMMENT     OS   Artificial Sequence
           PN   JP 2002034598-A/7
           PD   05-FEB-2002
           PF   27-JUL-2000 JP 2000226912
           PI   SATOKO YOSHIGA,YUTAKA TAKARADA,TOSHIYA AONO,MASAYA SEGAWA PC
           C12Q1/68,C12N9/22,C12N15/09,C12N15/00
           CC   Description of Artificial Sequence:primer
           FH   Key             Location/Qualifiers
           FT   source          1. .26
           FT                   /organism='Artificial Sequence'.
EATURES              Location/Qualifiers
    source           1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
RIGIN

 Query Match             100.0%;  Score 18;  DB 2;  Length 26;
 Best Local Similarity   100.0%;  Pred. No. 1.3;
 Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Y           1 CATCGCCTGGACTCCGAG 18
              ||||||||||||||||||
D           9 CATCGCCTGGACTCCGAG 26


ESULT 2
R530447
OCUS       AR530447                 21 bp    DNA     linear   PAT 08-OCT-2004
EFINITION  Sequence 1650 from patent US 6727063.
CCESSION   AR530447
ERSION     AR530447.1  GI:53918884
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 21)
 AUTHORS   Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
           McCarthy,J.J.
 TITLE     Single nucleotide polymorphisms in genes
 JOURNAL   Patent: US 6727063-A 1650 27-APR-2004;
           Millennium Pharmaceuticals, Inc. and Whitehead Institute for
           Biomedical Research; Cambridge, MA
EATURES              Location/Qualifiers
    source           1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"
RIGIN

 Query Match             100.0%;  Score 18;  DB 2;  Length 21;
 Best Local Similarity   94.4%;  Pred. No. 2;
 Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Y           1 CATCGCCTGGACTCCGAG 18
              |||||||:||||||||||
```

ESULT 3
X096472
OCUS AX096472 21 bp DNA linear PAT 30-MAR-2001
EFINITION Sequence 1650 from Patent WO0118250.
CCESSION AX096472
ERSION AX096472.1 GI:13512726
EYWORDS .
OURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
EFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
Mccarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1650 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
EATURES Location/Qualifiers
source 1. .21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
RIGIN

Query Match 100.0%; Score 18; DB 2; Length 21;
Best Local Similarity 94.4%; Pred. No. 2;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAG 18
|||||||:||||||||||
O 4 CATCGCCYGGACTCCGAG 21

!--EndFragment-->

!--StartFragment-->RESULT 1
S-09-304-232-896
 Sequence 896, Application US/09304232
 Patent No. 6525185
 GENERAL INFORMATION:
  APPLICANT: Fan, Jian Bing
  APPLICANT: Chakravarti, Aravinda
  APPLICANT: Halushka, Marc Kenneth
  APPLICANT: Case Western Reserve University School of Medicine
  APPLICANT: Affymetrix, Inc.
  TITLE OF INVENTION: Polymorphisms Associated With
  TITLE OF INVENTION: Hypertension
  FILE REFERENCE: 018547-034210US
  CURRENT APPLICATION NUMBER: US/09/304,232
  CURRENT FILING DATE: 1999-05-03
  EARLIER APPLICATION NUMBER: US 60/084,641
  EARLIER FILING DATE: 1998-05-07
  NUMBER OF SEQ ID NOS: 909
  SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 896
   LENGTH: 29
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: ADRB3EX1 416
S-09-304-232-896

 Query Match   100.0%; Score 20; DB 3; Length 29;
 Best Local Similarity   95.0%; Pred. No. 2.1;
 Matches   19; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

y   1 CATCGCCTGGACTCCGAGAC 20
             ||||||:||||||||||||
c   8 CATCGCCYGGACTCCGAGAC 27

ESULT 2
S-09-657-472-1650
 Sequence 1650, Application US/09657472
 Patent No. 6727063
 GENERAL INFORMATION:
  APPLICANT: Lander, Eric S.
  APPLICANT: Cargill, Michele
  APPLICANT: Ireland, James S.
  APPLICANT: Bolk, Stacey
  APPLICANT: Daley, George Q.
  APPLICANT: McCarthy, Jeanette J.
  TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
  FILE REFERENCE: 2825.1027-001
  CURRENT APPLICATION NUMBER: US/09/657,472
  CURRENT FILING DATE: 2000-09-07
  PRIOR APPLICATION NUMBER: US 60/153,357
  PRIOR FILING DATE: 1999-09-10
  PRIOR APPLICATION NUMBER: US 60/220,947
  PRIOR FILING DATE: 2000-07-26
  PRIOR APPLICATION NUMBER: US 60/225,724
  PRIOR FILING DATE: 2000-08-16
  NUMBER OF SEQ ID NOS: 2551
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1650
   LENGTH: 21
   TYPE: DNA
   ORGANISM: Homo sapiens
S-09-657-472-1650

 Query Match   88.0%; Score 17.6; DB 3; Length 21;
 Best Local Similarity   94.4%; Pred. No. 20;
 Matches   17; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

y   1 CATCGCCTGGACTCCGAG 18
             ||||||| |||||||||

ESULT 3
3-09-657-472-1651
Sequence 1651, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1651
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
3-09-657-472-1651

Query Match 88.0%; Score 17.6; DB 3; Length 21;
Best Local Similarity 94.4%; Pred. No. 20;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 3 TCGCCTGGACTCCGAGAC 20
||||||||||:|||||||
C 1 TCGCCTGGACWCCGAGAC 18

ESULT 4
3-08-446-530-5/c
Sequence 5, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,530
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-446-530-5

Query Match 85.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGA 17
||||||||||||||||
o 17 CATCGCCTGGACTCCGA 1

ESULT 5
3-08-446-530-7
Sequence 7, Application US/08446530
Patent No. 5766851
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,530
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-446-530-7

Query Match 85.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGA 17
||||||||||||||||

ESULT 6
3-09-097-562-5/c
Sequence 5, Application US/09097562
Patent No. 5877283
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,530
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-09-097-562-5

Query Match 85.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGA 17
||||||||||||||||
D 17 CATCGCCTGGACTCCGA 1

ESULT 7
3-09-097-562-7
Sequence 7, Application US/09097562
Patent No. 5877283
GENERAL INFORMATION:
APPLICANT: Shuldiner, Alan R.
APPLICANT: Walston, Jeremy
APPLICANT: Silver, Kristi
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
TITLE OF INVENTION: II DIABETES MELLITUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:

CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,530
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/048001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-09-097-562-7

Query Match 85.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGA 17
||||||||||||||||
D 1 CATCGCCTGGACTCCGA 17

!--EndFragment-->

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104100_us-10-553-509-9.szlm60.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104100_us-10-53-509-9.szlm60.rng.

tart | next page

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 05:57:43 ; Search time 241.124 Seconds
(without alignments)
578.313 Million cell updates/sec

itle: US-10-553-509-9
erfect score: 20
equence: 1 catcgcctggactccgagac 20

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters: 5397982

inimum DB seq length: 0
aximum DB seq length: 60

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	12	ABT02448	Adb02448 Fluoresc

	3	20	100.0	34	13	ADT93453 Adt93453 Human bet
	4	19.6	100.0	29	3	AAA04696 Aaa04696 Polymorph
	5	19.6	100.0	41	6	ABK50101 Abk50101 Nucleic a
	6	18.4	92.0	25	12	ADO26526 Ado26526 Novel hyb
	7	18.4	92.0	34	13	ADT93454 Adt93454 Human bet
	8	18.4	92.0	41	6	ABK50104 Abk50104 Sense str
	9	18	90.0	18	13	ADT93450 Adt93450 Fluoresce
C	10	18	90.0	18	14	AEC91756 Aec91756 Probe 3T-
	11	18	90.0	21	4	AAF96886 Aaf96886 Human gen
	12	18	90.0	21	4	AAF96885 Aaf96885 Human gen
	13	18	90.0	26	6	ABL40567 Abl40567 Primer #7
	14	17.6	88.0	21	3	AAC73164 Aac73164 SNP flank
	15	17	85.0	17	2	AAT58989 Aat58989 Obesity a
C	16	17	85.0	17	2	AAT58987 Aat58987 Obesity a
C	17	17	85.0	17	14	AEC91758 Aec91758 Probe 5T-
	18	17	85.0	19	6	ABK50102 Abk50102 Allele sp
	19	16.4	82.0	19	13	ADT93446 Adt93446 Fluoresce
	20	16.4	82.0	25	6	ABL40568 Abl40568 Primer #8
	21	16	80.0	16	13	ADT93451 Adt93451 Fluoresce
C	22	15.4	77.0	17	2	AAT58988 Aat58988 Obesity a
	23	15.4	77.0	17	2	AAT58990 Aat58990 Obesity a
	24	15.4	77.0	21	14	AEC91760 Aec91760 Probe 3T-
	25	15.4	77.0	51	4	AAH90342 Aah90342 Human clo
	26	15.4	77.0	51	4	AAH90341 Aah90341 Human clo
	27	15	75.0	15	13	ADT93452 Adt93452 Fluoresce
	28	14.8	74.0	25	9	ACK05002 Ack05002 Human mic
C	29	14.4	72.0	25	9	ACI43012 Aci43012 Human mic
C	30	14.4	72.0	25	9	ACI43640 Aci43640 Human mic
	31	14.4	72.0	25	9	ACK29689 Ack29689 Human mic
	32	14.2	71.0	25	9	ACI08822 Aci08822 Human mic
C	33	14.2	71.0	48	10	ADJ80399 Adj80399 Hybrid hu
C	34	14	70.0	14	13	ADU50896 Adu50896 Human bet
C	35	14	70.0	14	14	ADZ42342 Adz42342 FAM probe
	36	14	70.0	41	6	ABZ46998 Abz46998 Human ATP
	37	14	70.0	41	6	ABZ46999 Abz46999 Human ATP
	38	13.8	69.0	21	13	ADU31703 Adu31703 Knock-dow
	39	13.6	68.0	25	12	ADP13719 Adp13719 Renal cel
	40	13.6	68.0	34	2	AAV33317 Aav33317 Anti-CD23
C	41	13.6	68.0	50	4	AAH89585 Aah89585 Human col
C	42	13.6	68.0	51	4	AAL27124 Aal27124 Human SNP
	43	13.6	68.0	60	14	AED87834 Aed87834 Rabbit ty
	44	13.4	67.0	16	13	ADT93445 Adt93445 Fluoresce
C	45	13.4	67.0	19	10	ADF83960 Adf83960 Human bre

ALIGNMENTS

```
ESULT 1
DT93449
D   ADT93449 standard; DNA; 20 BP.
K
C   ADT93449;
K
T   13-JAN-2005  (first entry)
K
E   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 9.
K
W   SNP detection; beta3 adrenaline receptor; ss; probe.
K
S   Homo sapiens.
K
H   Key             Location/Qualifiers
T   modified_base   1
T                   /*tag=  a
T                   /mod_base= OTHER
T                   /note= "OTHER = Linked to BODIPY FL group"
T   modified_base   20
T                   /*tag=  b
T                   /mod_base= OTHER
```

/Note= "ARKR - Linked to 1 group"

XX
WO2004092385-A1.
XX
28-OCT-2004.
XX
16-APR-2004; 2004WO-JP005525.
XX
18-APR-2003; 2003JP-00114381.
XX
(ARKR-) ARKRAY INC.
XX
Hirai M;
XX
WPI; 2004-784610/77.
XX
Nucleic acid probe useful for detecting mutation in beta3 adrenaline
receptor gene having single nucleotide polymorphism, labeled at terminal
with fluorescent dye and shows decrease in fluorescence of fluorescent
dye upon hybridization.
XX
Claim 2; SEQ ID NO 9; 31pp; Japanese.
XX
The invention relates to a novel nucleic acid probe which is labelled at
a terminal with a fluorescent dye, whereby a decrease in the fluorescence
of the fluorescent dye is observed upon hybridisation. The probe
comprises a base sequence derived from a fully defined sequence of 1227
nucleotides as given in the specification and being labelled at the 3' or
5' end with a fluorescent dye. The probe of the invention may be useful
for detecting a mutation or single nucleotide polymorphism (SNP) in the
beta3 adrenaline receptor (B3AR) gene. The probe is effective in
detecting a B3AR Trp64Arg mutation within a short time whilst risk of
contamination of the amplified product is prevented and the process is
automated. The current sequence is that of the fluorescent-labelled probe
(SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
receptor (B3AR) T190 variant DNA.
XX
Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAGAC 20
||||||||||||||||||||
o 1 CATCGCCTGGACTCCGAGAC 20

ESULT 2
DO26525
ADO26525 standard; DNA; 25 BP.
XX
ADO26525;
XX
12-AUG-2004 (first entry)
XX
Novel hybridisation detection-related oligonucleotide SeqID1.
XX
hybridisation detection; immobilised probe; AC impedance;
foetal genome analysis; ss.
XX
Unidentified.
XX
WO2004044570-A1.
XX
27-MAY-2004.
XX
30-SEP-2003; 2003WO-JP012499.
XX
14-NOV-2002; 2002JP-00331059.

A (COSE-) COSEL CO LTD.
A (TATE-) TATEYAMA KAGAKU IND CO LTD.
A (TOXX) TOYO KAKO CO LTD.
K
I Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
I Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
K
R WPI; 2004-420427/39.
K
T Detection of hybridization of an immobilized probe to a target nucleic
T acid by measuring AC impedance across the carrier surface for specific
T gene detection in investigation and diagnosis of disease.
K
S Example; SEQ ID NO 1; 33pp; Japanese.
K
C This invention relates to a novel method of detecting hybridisation of an
C immobilised probe to a target nucleic acid using measurement of AC
C impedance. Detection of specific genes and gene sequences in nucleic acid
C samples (such as samples of genomic DNA) may be useful for diagnosis,
C prediction and prevention of genetic disorders and analysis of foetal
C genome. Hybridisation is detected with high accuracy and sensitivity
C without the use of dyes. The present sequence is that of an
C oligonucleotide which was used in the exemplification of the invention.
K
S Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAGAC 20
||||||||||||||||||||
D 6 CATCGCCTGGACTCCGAGAC 25

ESULT 3
DT93453
D ADT93453 standard; DNA; 34 BP.
K
C ADT93453;
K
T 13-JAN-2005 (first entry)
K
E Human beta3 adrenaline receptor (B3AR) T190 variant DNA fragment.
K
K single nucleotide polymorphism; SNP; SNP detection;
K beta3 adrenaline receptor; ds.
K
S Homo sapiens.
K
H Key Location/Qualifiers
T variation replace(19,C)
T /*tag= a
T /standard_name= "Single nucleotide polymorphism"
K
N WO2004092385-A1.
K
D 28-OCT-2004.
K
F 16-APR-2004; 2004WO-JP005525.
K
R 18-APR-2003; 2003JP-00114381.
K
A (ARKR-) ARKRAY INC.
K
I Hirai M;
K
R WPI; 2004-784610/77.
K
T Nucleic acid probe useful for detecting mutation in beta3 adrenaline

receptor gene having single nucleotide polymorphism, labeled at terminal
with fluorescent dye and shows decrease in fluorescence of fluorescent
dye upon hybridization.

Example 1; Fig 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at
a terminal with a fluorescent dye, whereby a decrease in the fluorescence
of the fluorescent dye is observed upon hybridisation. The probe
comprises a base sequence derived from a fully defined sequence of 1227
nucleotides as given in the specification and being labelled at the 3' or
5' end with a fluorescent dye. The probe of the invention may be useful
for detecting a mutation or single nucleotide polymorphism (SNP) in the
beta3 adrenaline receptor (B3AR) gene. The probe is effective in
detecting a B3AR Trp64Arg mutation within a short time whilst risk of
contamination of the amplified product is prevented and the process is
automated. The current sequence is that of the human beta3 adrenaline
receptor (B3AR) T190 variant DNA fragment of the invention.

Sequence 34 BP; 5 A; 13 C; 9 G; 7 T; 0 U; 0 Other;

```
 Query Match             100.0%;  Score 20;  DB 13;  Length 34;
 Best Local Similarity   100.0%;  Pred. No. 6;
 Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Y          1 CATCGCCTGGACTCCGAGAC 20
             ||||||||||||||||||||
D         12 CATCGCCTGGACTCCGAGAC 31
```

ESULT 4
AA04696
AAA04696 standard; DNA; 29 BP.

AAA04696;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene ADRB3.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
polycystic kidney disease; von Willebrands disease; forensic; human;
tuberous sclerosis; hereditary hemorrhagica telangiectasia;
familial colonic polyposis; osteogenesis imperfecta; porphyria;
Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999;   99EP-00250150.

07-MAY-1998;   98US-0084641P.
03-MAY-1999;   99US-00304232.

(AFFY-) AFFYMETRIX INC.
(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of
hypertension.

Disclosure; Page 45; 53pp; English.

C The invention provides polymorphic fragments of genes associated with
C hypertension. The nucleic acids including the polymorphic sites can be
C used as probes or primers for expressing variant proteins. Detection of
C the polymorphisms is useful in designing prophylactic and therapeutic
C regimes customized to underlying abnormalities. The polymorphisms can be
C used for association studies for hypertension, and in hypertension
C diagnostic assays. Where the polymorphisms have strong correlation with
C hypertension, within a gene, they are likely to have a causative role in
C hypertension. This information can be used to find the precise role of a
C polymorphism in the disease, and this can be used to identify potential
C drugs which combat the disease. The polymorphisms can be tested for
C association with other diseases e.g. agammaglobulinemia, diabetes
C insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
C syndrome, Fabrys disease, familial hypercholesterolemia, polycystic
C kidney disease, hereditary spherocytosis, von Willebrands disease,
C tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
C colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
C acute intermittent porphyria. The polymorphic forms can also be used in
C forensics to identify individuals
XX
SQ Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 3; Length 29;
Best Local Similarity 95.0%; Pred. No. 9.4;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAGAC 20
||||||:||||||||||||
D 8 CATCGCCYGGACTCCGAGAC 27

ESULT 5
3K50101
D ABK50101 standard; DNA; 41 BP.
XX
C ABK50101;
XX
I 15-JUL-2002 (first entry)
XX
E Nucleic acid sequence used for sequence formatting.
XX
W Optimal reagent oligonucleotide; target nucleic acid evaluation;
W target feature; exclusion value; ranking value; sequence window;
W sequence formatting; ds.
XX
S Synthetic.
XX
N WO200229379-A2.
XX
D 11-APR-2002.
XX
F 04-OCT-2001; 2001WO-US031037.
XX
R 04-OCT-2000; 2000US-0237383P.
XX
A (CELA-) CELADON LAB INC.
XX
I Peterson RJ;
XX
R WPI; 2002-340129/37.
XX
T Determining an optimal reagent oligonucleotide for evaluating a target
T nucleic acid having a target feature, involves defining a set of
T exclusion values and/or ranking values specific to a biochemical method.
XX
S Example; Fig 1B; 91pp; English.
XX
C The present invention relates to a new method for determining an optimal
C reagent oligonucleotide for evaluating a target nucleic acid having a
C target feature. The method comprises defining a set of exclusion values
C and/or ranking values specific to the method, defining a sequence window

adjacent to the target, and generating candidate reagent oligonucleotides
complementary to the sense and/or antisense strands of the target within
the window. The method can be used for determining an optimal reagent
oligonucleotide sequence for use in a biochemical method for evaluating a
target nucleic acid sequence having a target feature. The present nucleic
acid sequence represent a DNA molecule used in the methods of the
invention for nucleic acid sequence formatting
XX
Sequence 41 BP; 7 A; 15 C; 11 G; 7 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 6; Length 41;
Best Local Similarity 95.0%; Pred. No. 9.6;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CATCGCCTGGACTCCGAGAC 20
||||||:||||||||||||
D 14 CATCGCCYGGACTCCGAGAC 33

ESULT 6
DO26526
ID ADO26526 standard; DNA; 25 BP.
XX
AC ADO26526;
XX
DT 12-AUG-2004 (first entry)
XX
DE Novel hybridisation detection-related oligonucleotide SeqID2.
XX
KW hybridisation detection; immobilised probe; AC impedance;
KW foetal genome analysis; ss.
XX
OS Unidentified.
XX
PN WO2004044570-A1.
XX
PD 27-MAY-2004.
XX
PF 30-SEP-2003; 2003WO-JP012499.
XX
PR 14-NOV-2002; 2002JP-00331059.
XX
PA (TOYA-) TOYAMA PREFECTURE.
PA (COSE-) COSEL CO LTD.
PA (TATE-) TATEYAMA KAGAKU IND CO LTD.
PA (TOXX) TOYO KAKO CO LTD.
XX
PI Terasawa T, Kadosaki M, Makimura M, Fujiki S, Tanino K;
PI Nakagawa A, Mizuhara T, Mizushima M, Nakada M;
XX
DR WPI; 2004-420427/39.
XX
PT Detection of hybridization of an immobilized probe to a target nucleic
PT acid by measuring AC impedance across the carrier surface for specific
PT gene detection in investigation and diagnosis of disease.
XX
PS Example; SEQ ID NO 2; 33pp; Japanese.
XX
CC This invention relates to a novel method of detecting hybridisation of an
CC immobilised probe to a target nucleic acid using measurement of AC
CC impedance. Detection of specific genes and gene sequences in nucleic acid
CC samples (such as samples of genomic DNA) may be useful for diagnosis,
CC prediction and prevention of genetic disorders and analysis of foetal
CC genome. Hybridisation is detected with high accuracy and sensitivity
CC without the use of dyes. The present sequence is that of an
CC oligonucleotide which was used in the exemplification of the invention.
XX
SQ Sequence 25 BP; 4 A; 10 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 12; Length 25;
Best Local Similarity 95.0%; Pred. No. 36;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAGAC 20
||||||| ||||||||||||
o 6 CATCGCCCGGACTCCGAGAC 25

ESULT 7
DT93454
D ADT93454 standard; DNA; 34 BP.
K
C ADT93454;
K
R 13-JAN-2005 (first entry)
K
E Human beta3 adrenaline receptor (B3AR) C190 variant DNA fragment.
K
W single nucleotide polymorphism; SNP; SNP detection;
W beta3 adrenaline receptor; ds.
K
S Homo sapiens.
K
H Key Location/Qualifiers
F variation replace(19,T)
F /*tag= a
F /standard_name= "Single nucleotide polymorphism"
K
N WO2004092385-A1.
K
D 28-OCT-2004.
K
P 16-APR-2004; 2004WO-JP005525.
K
R 18-APR-2003; 2003JP-00114381.
K
A (ARKR-) ARKRAY INC.
K
I Hirai M;
K
R WPI; 2004-784610/77.
K
F Nucleic acid probe useful for detecting mutation in beta3 adrenaline
F receptor gene having single nucleotide polymorphism, labeled at terminal
F with fluorescent dye and shows decrease in fluorescence of fluorescent
F dye upon hybridization.
K
S Example 1; Fig 1; 31pp; Japanese.
K
C The invention relates to a novel nucleic acid probe which is labelled at
C a terminal with a fluorescent dye, whereby a decrease in the fluorescence
C of the fluorescent dye is observed upon hybridisation. The probe
C comprises a base sequence derived from a fully defined sequence of 1227
C nucleotides as given in the specification and being labelled at the 3' or
C 5' end with a fluorescent dye. The probe of the invention may be useful
C for detecting a mutation or single nucleotide polymorphism (SNP) in the
C beta3 adrenaline receptor (B3AR) gene. The probe is effective in
C detecting a B3AR Trp64Arg mutation within a short time whilst risk of
C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the human beta3 adrenaline
C receptor (B3AR) C190 variant DNA fragment of the invention.
K
Q Sequence 34 BP; 5 A; 14 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 13; Length 34;
Best Local Similarity 95.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CATCGCCTGGACTCCGAGAC 20
||||||| ||||||||||||
o 12 CATCGCCCGGACTCCGAGAC 31

ESULT 8
3K50104
D ABK50104 standard; DNA; 41 BP.
K
C ABK50104;
K
R 15-JUL-2002 (first entry)
K
E Sense strand of target nucleic acid.
K
W Optimal reagent oligonucleotide; target nucleic acid evaluation;
W target feature; exclusion value; ranking value; sequence window;
W single nucleotide polymorphism; SNP; ds.
K
S Synthetic.
K
H Key   Location/Qualifiers
F variation   replace(21,T)
F   /*tag= a
F   /standard_name= "Single nucleotide polymorphism"
K
N WO200229379-A2.
K
D 11-APR-2002.
K
F 04-OCT-2001; 2001WO-US031037.
K
R 04-OCT-2000; 2000US-0237383P.
K
A (CELA-) CELADON LAB INC.
K
I Peterson RJ;
K
R WPI; 2002-340129/37.
K
F Determining an optimal reagent oligonucleotide for evaluating a target
F nucleic acid having a target feature, involves defining a set of
F exclusion values and/or ranking values specific to a biochemical method.
K
S Example; Fig 4A; 91pp; English.
K
C The present invention relates to a new method for determining an optimal
C reagent oligonucleotide for evaluating a target nucleic acid having a
C target feature. The method comprises defining a set of exclusion values
C and/or ranking values specific to the method, defining a sequence window
C adjacent to the target, and generating candidate reagent oligonucleotides
C complementary to the sense and/or antisense strands of the target within
C the window. The method can be used for determining an optimal reagent
C oligonucleotide sequence for use in a biochemical method for evaluating a
C target nucleic acid sequence having a target feature. The present nucleic
C acid sequence represent the sense strand of a target nucleic acid. This
C sequence was used in the methods of the invention in a sequence window
K
Q Sequence 41 BP; 7 A; 16 C; 11 G; 7 T; 0 U; 0 Other;

 Query Match   92.0%; Score 18.4; DB 6; Length 41;
 Best Local Similarity   95.0%; Pred. No. 37;
 Matches   19; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Y   1 CATCGCCTGGACTCCGAGAC 20
             ||||||| ||||||||||||
D   14 CATCGCCCGGACTCCGAGAC 33

ESULT 9
DT93450
D ADT93450 standard; DNA; 18 BP.
K
C ADT93450;
K

XX
DE   Fluorescent probe targeted to human B3AR T190 variant DNA - SEQ ID 10.
XX
KW   SNP detection; beta3 adrenaline receptor; ss; probe.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   modified_base   1
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "OTHER = Linked to BODIPY FL group"
FT   modified_base   18
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "OTHER = Optionally linked to P group"
XX
PN   WO2004092385-A1.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-JP005525.
XX
PR   18-APR-2003; 2003JP-00114381.
XX
PA   (ARKR-) ARKRAY INC.
XX
PI   Hirai M;
XX
DR   WPI; 2004-784610/77.
XX
PT   Nucleic acid probe useful for detecting mutation in beta3 adrenaline
PT   receptor gene having single nucleotide polymorphism, labeled at terminal
PT   with fluorescent dye and shows decrease in fluorescence of fluorescent
PT   dye upon hybridization.
XX
PS   Claim 2; SEQ ID NO 10; 31pp; Japanese.
XX
CC   The invention relates to a novel nucleic acid probe which is labelled at
CC   a terminal with a fluorescent dye, whereby a decrease in the fluorescence
CC   of the fluorescent dye is observed upon hybridisation. The probe
CC   comprises a base sequence derived from a fully defined sequence of 1227
CC   nucleotides as given in the specification and being labelled at the 3' or
CC   5' end with a fluorescent dye. The probe of the invention may be useful
CC   for detecting a mutation or single nucleotide polymorphism (SNP) in the
CC   beta3 adrenaline receptor (B3AR) gene. The probe is effective in
CC   detecting a B3AR Trp64Arg mutation within a short time whilst risk of
CC   contamination of the amplified product is prevented and the process is
CC   automated. The current sequence is that of the fluorescent-labelled probe
CC   (SEQ ID 5) of the invention which was targeted to human beta3 adrenaline
CC   receptor (B3AR) T190 variant DNA.
XX
SQ   Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

 Query Match   90.0%; Score 18; DB 13; Length 18;
 Best Local Similarity   100.0%; Pred. No. 56;
 Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCGAG 18
              ||||||||||||||||||
Db   1 CATCGCCTGGACTCCGAG 18

RESULT 10
AEC91756/c
ID   AEC91756 standard; DNA; 18 BP.
XX
AC   AEC91756;
XX
DT   01-DEC-2005 (first entry)

E Probe 3T-B3AR-w-IMS-R1-18 SEQ ID NO:32.
K
W DNA detection; SNP detection; probe; ss.
K
S Synthetic.
K
N JP2005261354-A.
K
D 29-SEP-2005.
K
F 19-MAR-2004; 2004JP-00080974.
K
R 19-MAR-2004; 2004JP-00080974.
K
A (KYOT-) KYOTO DAIICHI KAGAKU KK.
K
I Inose K;
K
R WPI; 2005-662138/68.
K
P Detecting target nucleic acid, involves detecting target based on change
P of fluorescence intensity due to formation or dissociation of hybrid of
P target nucleic acid and hybridization probe having 5-carboxy fluorescein.
K
S Example 10; SEQ ID NO 32; 28pp; Japanese.
K
C The invention relates to a method (M1) for detecting a target nucleic
C acid. (M1) involves measuring the change of fluorescence intensity due to
C formation or dissociation of the hybrid of the hybridization probe
C comprising a labeled terminal portion, and a target nucleic acid, and
C detecting the target nucleic acid based on the change, where the
C hybridization probe is labeled using the fluorescent pigment chosen from
C 6-carboxy tetramethyl rhodamine (TAMRA), 4,4-difluoro-5,7-dimethyl-4-bora
C -3a,4a-diaza-s-indacene-3-propionic acid (BODIPY FL), 6-carboxy-4',5'-
C dichloro-2',7'-dimethoxy fluorescein (JOE), 5-carboxy fluorescein (FAM),
C 5-carboxy-X-rhodamine (ROX) and [(3,6,8-tri-sulfo 1-pyrenyl)oxy]aceto
C hydrazide (Cascade blue). Also described: (1) a real-time PCR method
C (M2), which involves carrying out real-time PCR using the hybridization
C probe labeled with the fluorescent pigment, where the hybridization probe
C is the probe labeled at its terminal with the fluorescent pigment chosen
C from TAMRA, BODIPY FL, JOE, FAM, ROX and Cascade blue; and (2) a melting-
C curve analysis (M3), which involves using the hybridization probe labeled
C with the fluorescent pigment, where the hybridization probe is the probe
C labeled at its terminal with the fluorescent pigment chosen from TAMRA,
C BODIPY FL, JOE, FAM, ROX and Cascade blue. (M1) is useful for detecting a
C target nucleic acid. (M1)-(M3) are useful for detecting mutations in a
C target nucleic acid and single nucleotide polymorphisms (SNPs), and in
C measurement of the ratio of normal type DNA and variant DNA. (M1) enables
C detection of the nucleic acid by fluorescent detection method, easily and
C cost effectively. The present sequence represents a probe used in an
C example from the present invention.
K
S Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

 Query Match   90.0%; Score 18; DB 14; Length 18;
 Best Local Similarity   100.0%; Pred. No. 56;
 Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   2 ATCGCCTGGACTCCGAGA 19
             ||||||||||||||||||
D   18 ATCGCCTGGACTCCGAGA 1

ESULT 11
AF96886
D AAF96886 standard; DNA; 21 BP.
K
C AAF96886;
K
R 18-NOV-2004 (revised)

XX
DE   Human gene single nucleotide polymorphism #1647.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   variation   11
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 159; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
CC
CC   Revised record issued on 18-NOV-2004 : The variantion feature was
CC   incorrectly given a captial V
XX
SQ   Sequence 21 BP; 3 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

 Query Match   90.0%; Score 18; DB 4; Length 21;
 Best Local Similarity   100.0%; Pred. No. 57;
 Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Y   3 TCGCCTGGACTCCGAGAC 20
             ||||||||||||||||||
Db   1 TCGCCTGGACTCCGAGAC 18

ESULT 12
AF96885
ID   AAF96885 standard; DNA; 21 BP.

XX

RL 18-NOV-2004 (revised)
RL 06-JUN-2001 (first entry)

XX

DE Human gene single nucleotide polymorphism #1646.

XX

KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.

XX

OS Homo sapiens.
OS Unidentified.

XX

FH Key Location/Qualifiers
FT variation 11
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"

XX

PN WO200118250-A2.

XX

PD 15-MAR-2001.

XX

PF 07-SEP-2000; 2000WO-US024503.

XX

PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.

XX

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;

XX

DR WPI; 2001-226749/23.

XX

PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.

XX

PS Example; Page 159; 242pp; English.

XX

CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPS shown in the specification
CC
CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a captial V

XX

SQ Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCGCCTGGACTCCGAG 18
||||||||||||||||||
Db 4 CATCGCCTGGACTCCGAG 21

RESULT 13

ID   ABL40567 standard; DNA; 26 BP.
XX
AC   ABL40567;
XX
DT   17-JUN-2002 (first entry)
XX
DE   Primer #7 used in a base polymorphism detection method.
XX
KW   Polymorphism; nucleic acid detection; endonuclease; probe; ADRB2;
KW   hybridisation; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2002034598-A.
XX
PD   05-FEB-2002.
XX
PF   27-JUL-2000; 2000JP-00226912.
XX
PR   27-JUL-2000; 2000JP-00226912.
XX
PA   (TOYM) TOYOBO KK.
XX
DR   WPI; 2002-298820/34.
XX
PT   Detection of base polymorphism.
XX
PS   Disclosure; Page 10; 10pp; Japanese.
XX
CC   The invention relates to a method for detecting base polymorphism. The
CC   method involves (1) amplifying the nucleic acid fragment containing base
CC   polymorphism of the specific nucleic acid sequence; (2) hybridising the
CC   amplified nucleic acid with at least two polymorphism-specific probes;
CC   (3) treating with RNA-selective cleavage endonuclease; (4) measuring
CC   detecting signals of each probe; and (5) identifying polymorphism by the
CC   ratio of each detecting signals. The probe can be used for detecting base
CC   polymorphism. The present sequence represents a PCR primer used in the
CC   course of the invention
XX
SQ   Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

 Query Match   90.0%; Score 18; DB 6; Length 26;
 Best Local Similarity   100.0%; Pred. No. 57;
 Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CATCGCCTGGACTCCGAG 18
              ||||||||||||||||||
Db   9 CATCGCCTGGACTCCGAG 26

RESULT 14
AAC73164
ID   AAC73164 standard; DNA; 21 BP.
XX
AC   AAC73164;
XX
DT   02-FEB-2001 (first entry)
XX
DE   SNP flanking sequence #24 used in multiplexing PCR/SBE assay.
XX
KW   Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW   polymorphic locus; single nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   WO200058516-A2.
XX
PD   05-OCT-2000.
XX
PF   27-MAR-2000; 2000WO-US008069.

RR 26-MAR-1999; 99US-0126473P.
RR 23-JUN-1999; 99US-0140359P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
PS Example 7; Page 50; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci

tart | next page

#--StartFragment-->RESULT 1
3-09-304-232-896
Sequence 896, Application US/09304232
Patent No. 6525185
GENERAL INFORMATION:
APPLICANT: Fan, Jian Bing
APPLICANT: Chakravarti, Aravinda
APPLICANT: Halushka, Marc Kenneth
APPLICANT: Case Western Reserve University School of Medicine
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Polymorphisms Associated With
TITLE OF INVENTION: Hypertension
FILE REFERENCE: 018547-034210US
CURRENT APPLICATION NUMBER: US/09/304,232
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: US 60/084,641
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 909
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 896
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ADRB3EX1 416
3-09-304-232-896

Query Match 100.0%; Score 20; DB 3; Length 29;
Best Local Similarity 95.0%; Pred. No. 8.1;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 1 CGTGGCCATCGCCCGGACTC 20
||||||||||||:||||||
o 2 CGTGGCCATCGCCYGGACTC 21

ESULT 2
3-08-891-516-39
Sequence 39, Application US/08891516
Patent No. 6090552
GENERAL INFORMATION:
APPLICANT: NAZARENKO, Irina A.
APPLICANT: BHATNAGAR, Satish K.
APPLICANT: WINN-DEEN, Emily S.
APPLICANT: HOHMAN, Robert J.
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH MOLECULAR ENERGY TRANSFER LABELS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,516
FILING DATE: 11-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,034
FILING DATE: 11-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,487

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,667
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 079498/0109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
S-08-891-516-39

Query Match 85.0%; Score 17; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGTGGCCATCGCCCGGA 17
||||||||||||||||
D 11 CGTGGCCATCGCCCGGA 27

ESULT 3
S-08-837-034-39
Sequence 39, Application US/08837034
Patent No. 6117635
GENERAL INFORMATION:
APPLICANT: NAZARENKO, Irina A.
APPLICANT: BHATNAGAR, Satish K.
APPLICANT: WINN-DEEN, Emily S.
APPLICANT: HOHMAN, Robert J.
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH MOLECULAR ENERGY TRANSFER LABELS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,034
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,487
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,667
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 079498/0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-837-034-39

Query Match 85.0%; Score 17; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CGTGGCCATCGCCCGGA 17
||||||||||||||||
o 11 CGTGGCCATCGCCCGGA 27

ESULT 4
3-09-657-472-1650
Sequence 1650, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1650
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
3-09-657-472-1650

Query Match 83.0%; Score 16.6; DB 3; Length 21;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

y 4 GGCCATCGCCCGGACTC 20
||||||||||:||||||
o 1 GGCCATCGCCYGGACTC 17

ESULT 5
3-08-891-516-38
Sequence 38, Application US/08891516
Patent No. 6090552
GENERAL INFORMATION:
APPLICANT: NAZARENKO, Irina A.
APPLICANT: BHATNAGAR, Satish K.
APPLICANT: WINN-DEEN, Emily S.
APPLICANT: HOHMAN, Robert J.
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH MOLECULAR ENERGY TRANSFER LABELS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,516
FILING DATE: 11-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,034
FILING DATE: 11-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,487
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,667
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 079498/0109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-891-516-38

Query Match 77.0%; Score 15.4; DB 3; Length 27;
Best Local Similarity 94.1%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 CGTGGCCATCGCCCGGA 17
||||||||||||| |||
o 11 CGTGGCCATCGCCTGGA 27

ESULT 6
!--EndFragment-->

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104357_us-10-553-509-1_copy_180_240.rng.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104357_us-10-53-509-1_copy_180_240.rng.

tart | next page

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 14:32:10 ; Search time 299.969 Seconds
(without alignments)
1417.837 Million cell updates/sec

itle: US-10-553-509-1_COPY_180_240
erfect score: 61
equence: 1 ggccatcgcctggactccga.....tgttcgtgacttcgctggcc 61

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 5244920 seqs, 3486124231 residues

otal number of hits satisfying chosen parameters: 10489840

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	1003	12	AGV81002	Human gen

3	61	100.0	1185	14	AEA13746	Aea13746 Human bet
4	61	100.0	1227	2	AAQ55693	Aaq55693 DNA encod
5	61	100.0	1227	13	ADT93441	Adt93441 Human bet
6	61	100.0	1270	10	ACA56586	Aca56586 Human sig
7	61	100.0	1270	12	ADI56382	Adi56382 Human pol
8	61	100.0	2022	2	AAQ05731	Aaq05731 Beta 3 ad
9	61	100.0	2518	2	AAV23500	Aav23500 Human adr
10	61	100.0	2644	8	ABZ42630	Abz42630 Human bet
11	61	100.0	2644	11	ADN39372	Adn39372 Cancer/an
12	61	100.0	2644	12	ADO29809	Ado29809 Human GPC
13	61	100.0	2644	13	ADU50894	Adu50894 Human bet
14	61	100.0	2644	14	AEC83014	Aec83014 Breast ca
15	61	100.0	2644	14	AEE01346	Aee01346 Human G p
16	61	100.0	3682	2	AAQ65476	Aaq65476 Human bet
17	61	100.0	5669	13	ADU50893	Adu50893 Human bet
18	60.6	100.0	210	2	AAX11762	Aax11762 Human bia
19	60.6	100.0	420	14	AEC91757	Aec91757 Template
20	60.6	100.0	5669	14	ADZ42281	Adz42281 Human bet
21	60.6	100.0	10306	6	ABK11451	Abk11451 Human bet
22	59.4	97.4	100	14	AEC91742	Aec91742 Template
23	59.4	97.4	210	2	AAX12815	Aax12815 Human bia
24	59.4	97.4	1227	13	ADT93442	Adt93442 Human bet
25	57.8	94.8	2000	2	AAQ74367	Aaq74367 Bovine be
26	51.4	84.3	2649	2	AAV30469	Aav30469 Canine be
27	50.4	82.6	1203	12	ADO30100	Ado30100 Mouse GPC
28	50.4	82.6	1920	2	AAQ26808	Aaq26808 Murine ad
29	50.4	82.6	3437	2	AAQ65477	Aaq65477 Murine be
30	44.6	73.1	704	6	ABQ50482	Abq50482 Oligonucl
31	44.6	73.1	704	6	ABQ50483	Abq50483 Oligonucl
32	44.6	73.1	5832	6	ABN80280	Abn80280 Human che
33	44.6	73.1	7431	6	ABL32081	Abl32081 Human imm
34	44.6	73.1	7431	6	AAD28371	Aad28371 Human che
35	42.6	69.8	75	10	ADD32083	Add32083 Human bet
36	42.2	69.2	75	10	ADD32073	Add32073 Human bet
37	41	67.2	75	10	ADD32084	Add32084 Human bet
38	40.6	66.6	2040	6	ABK11513	Abk11513 Human bet
39	38.6	63.3	4749	3	AAZ98401	Aaz98401 Sheep bet
40	38.6	63.3	4749	6	ABK40733	Abk40733 Sheep bet
41	37	60.7	1845	3	AAZ98400	Aaz98400 Canine be
42	37	60.7	1845	6	ABK40732	Abk40732 Dog beta1
43	36	59.0	1584	3	AAZ98406	Aaz98406 Frog beta
44	36	59.0	1584	6	ABK40738	Abk40738 Frog beta
45	35.4	58.0	704	6	ABQ50484	Abq50484 Oligonucl

ALIGNMENTS

ESULT 1
CH91802
D ACH91802 standard; DNA; 1003 BP.
K
C ACH91802;
K
T 29-JUL-2004 (first entry)
K
E Human genome derived single exon probe #24997.
K
W Human; probe; ss; gene expression; single exon probe; microarray;
W alternative splicing event; genomic alteration.
K
S Homo sapiens.
K
N US2003194704-A1.
K
D 16-OCT-2003.
K
F 03-APR-2002; 2002US-00029386.
K

A (PENN/) PENN S G.
A (RANK/) RANK D R.
A (HANZ/) HANZEL D K.
X
I Penn SG, Rank DR, Hanzel DK;
X
R WPI; 2004-119264/12.
X
T New human genome-derived single exon nucleic acid probes useful for human
T gene expression analysis, for identifying or characterizing alternative
T splicing events, for assessing genomic alterations or as tools for
T surveying tissues.
X
S Claim 1; SEQ ID NO 24997; 80pp; English.
X
C The invention relates to a nucleic acid probe for measuring human gene
C expression, comprising any of the 27,400 fully defined nucleotide
C sequences in the specification, or their complements or fragments, and
C encoding at least 8 amino acids of any of the 6888 amino acid sequences
C fully defined in the specification. The probe is a single exon probe that
C hybridises under high stringency conditions to a nucleic acid molecule
C expressed in human cells or tissues. Also included are a spatially-
C addressable set of single exon nucleic acid probes for measuring human
C gene expression (comprising a plurality of single exon nucleic acid
C probes cited above, where each of the plurality of probes is separately
C and addressably isolatable or amplifiable from the plurality), a single
C exon microarray for measuring human gene expression, a method of
C measuring human gene expression, a vector comprising the single exon
C probe cited above, an ORF-encoded peptide comprising at least 8
C contiguous amino acids of any of the above- mentioned amino acid
C sequences (optionally with conservative amino acid substitutions), an
C isolated antibody that binds specifically to a peptide cited above,
C methods of selling and/or licensing single exon probes or microarrays to
C a customer desiring to measure gene expression, a method of providing
C human gene expression data by subscription, and a computer-readable
C storage medium which contains a database having a plurality of records
C (each record including data on the expression of a single exon probe
C cited above. The probe, methods and apparatus are useful in gene
C expression analysis. The probes may be used as tools for surveying
C tissues to detect the presence of expressed messages that contain their
C specific exon, or in constructing genome-derived single exon microarrays.
C In addition, the probes are used in identifying and characterising
C alternative splicing events, in detecting and characterising gross
C alterations in the genomic locus that includes their exon, in assessing
C smaller genomic alterations, in priming the synthesis of nucleic acids,
C or in expressing the ORF-encoded peptide. The present sequence is a human
C single exon probe of the invention. Note: The sequence data for this
C patent did not form part of the printed specification, but was obtained
C in electronic format directly from USPTO at
C seqdata.uspto.gov/sequence.html?DocID=20030194704
X
Q Sequence 1003 BP; 106 A; 369 C; 327 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 12; Length 1003;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o 169 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 228

y 61 C 61
|
o 229 C 229

ESULT 2
3X13060
D ABX13060 standard; DNA; 1185 BP.

XX

PT 29-AUG-2003 (revised)
PT 28-MAY-2003 (first entry)

XX

DE Human beta_3AR-V2R DNA.

XX

KW Human; G-protein coupled receptor; gene; ds; GPCR; palmitoylation site;
KW phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis;
KW atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain;
KW rheumatoid arthritis; obesity; Parkinson's disease; beta_3AR; V2R;
KW vasopressin V2R receptor; beta3-adrenergic receptor.

XX

OS Homo sapiens.
OS Chimeric.

XX

FH Key Location/Qualifiers
FT CDS 1. .1185
FT /*tag= a
FT /product= "Human beta_3AR-V2R"

XX

PN US2002106739-A1.

XX

PD 08-AUG-2002.

XX

PF 05-NOV-2001; 2001US-00993844.

XX

PR 03-NOV-2000; 2000US-0245772P.
PR 08-JAN-2001; 2001US-0260363P.

XX

PA (OAKL/) OAKLEY R H.
PA (BARA/) BARAK L S.
PA (LAPO/) LAPORTE S A.
PA (CARO/) CARON M G.

XX

PI Oakley RH, Barak LS, Laporte SA, Caron MG;

XX

DR WPI; 2002-690758/74.
DR P-PSDB; ABG75678.

XX

PT Modified G-protein coupled receptor useful for identifying an agonist,
PT inverse agonist or antagonist of the receptor, comprises a carboxyl
PT terminal having one or more clusters of phosphorylation.

XX

PS Disclosure; Fig 11; 57pp; English.

XX

CC The invention relates to a modified G-protein coupled receptor (GPCR)
CC comprising an NPXXY motif, and a carboxyl terminal tail which comprises a
CC putative site of palmitoylation and clusters of phosphorylation, and a
CC retained portion of a carboxyl terminal region of a GPCR portion fused to
CC a portion of the carboxyl terminal from a second GPCR, that comprises
CC phosphorylation clusters and a putative palmitoylation site 10-25 amino
CC acid residues downstream of a second NPXXY motif. The modified GPCR is
CC useful for screening compounds for GPCR activity which comprises
CC providing a cell that expresses at least one modified GPCR, where the
CC cell further comprises arrestin conjugated to a detectable molecule,
CC exposing the cell to the compound, detecting the location of the arrestin
CC within the cell, comparing the location of the arrestin within the cell
CC in the presence of the compound to the location of the arrestin within
CC the cell in the absence of the compound and correlating a difference
CC between the location of arrestin within the cell in the presence of the
CC compound and the presence of the location of the arrestin within the cell
CC in the absence of the compound. Preferably, the arrestin is detected in
CC endosomes. The GPCR and a nucleic acid encoding the modified GPCR are
CC useful for preventing and/or treating a disease associated with GPCR in
CC mammals, such as angina pectoris, atherosclerosis, asthma, emphysema,
CC rhinitis, inflammatory disease, rheumatoid arthritis, glaucoma, pain,
CC obesity or Parkinson's disease, by modulating GPCR activity and affinity
CC for arrestin. This sequence represents DNA encoding a chimeric receptor
CC polypeptide used in the scope of the invention. (Updated on 29-AUG-2003
CC to standardise OS field)

Sequence 1185 BP; 132 A; 446 C; 371 G; 236 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 6; Length 1185;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

Qy      61 C 61
           |
Db     240 C 240
```

ESULT 3
EA13746
AEA13746 standard; DNA; 1185 BP.
AEA13746;
28-JUL-2005 (first entry)
Human beta3AR - V2R chimeric DNA, SEQ ID NO: 13.
G-protein coupled receptor; gpcr; neurodegenerative disease;
neuroprotective; neurological disease; cardiovascular disease;
cardiovascular-gen.; nephrotropic; genitourinary disease; antidiabetic;
endocrine disease; gastrointestinal disease; metabolic disorder;
antiinflammatory; inflammation; ophthalmological; ocular disease;
gastrointestinal-gen.; analgesic; anorectic; nutritional disorder;
eating-disorders-gen.; psychiatric disorder; antidepressant;
tranquilizer; virucide; hematological disease; immune disorder;
infection; cytostatic; neoplasm; gene therapy; vasopressin V2 receptor;
beta 3 adrenoceptor; gene fusion; gene; ds.
Homo sapiens.

Key	Location/Qualifiers
CDS	1. .1185
	/*tag= a
	/product= "Beta3 adrenergic receptor-Vasopressin V2
	receptor fusion protein"

US2005106623-A1.
19-MAY-2005.
30-DEC-2004; 2004US-00026435.
03-NOV-2000; 2000US-0245772P.
08-JAN-2001; 2001US-0260363P.
05-NOV-2001; 2001US-00993844.
(OAKL/) OAKLEY R H.
(BARA/) BARAK L S.
(LAPO/) LAPORTE S A.
(CARO/) CARON M G.
Oakley RH, Barak LS, Laporte SA, Caron MG;
WPI; 2005-365814/37.
P-PSDB; AEA13740.
Screening compounds for G-protein coupled receptor agonist or antagonist
activity for preventing or treating, e.g. diabetes, comprises detecting
location of arrestin in the cell in the presence and absence of the
compound.
Disclosure; SEQ ID NO 13; 87pp; English.

C The present invention relates to modified G-protein coupled receptor
C (GPCR) proteins and their encoding polynucleotides. The invention is
C useful in screening compounds for GPCR agonist or antagonist activity for
C preventing or treating diseases associated with GPCR in mammals such as
C neurodegenerative disorders, cardiovascular diseases such as angina
C pectoris, essential hypertension, myocardial infarction, atherosclerosis,
C renal failure, diabetes, respiratory indications, inflammatory disease,
C glaucoma, gastrointestinal indications, pain, obesity, bulimia nervosa,
C depression, obsessive-compulsive disorder, Epstein-Barr infection and
C cancer. The invention is also useful in gene therapy. The present
C sequence is human beta-3 adrenergic receptor (beta3AR) - vasopressin V2
C receptor (V2R) chimeric DNA. This chimeric DNA consists of the DNA
C encoding amino acids 1-363 of human beta3AR and amino acids 366-394 of
C human V2R.
XX
SQ Sequence 1185 BP; 132 A; 446 C; 371 G; 236 T; 0 U; 0 Other;

Query Match   100.0%; Score 61; DB 14; Length 1185;
Best Local Similarity   100.0%; Pred. No. 1.2e-12;
Matches   61; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

Qy   61 C 61
              |
Db   240 C 240

RESULT 4
AAQ55693
ID AAQ55693 standard; DNA; 1227 BP.
XX
AC AAQ55693;
XX
DT 25-MAR-2003 (revised)
DT 23-JUL-1994 (first entry)
XX
DE DNA encoding the human beta-3 adrenergic receptor.
XX
KW Fusion protein; compounds; ss.
XX
OS Homo sapiens.
XX
PN WO9402590-A1.
XX
PD 03-FEB-1994.
XX
PF 16-JUL-1993; 93WO-US006733.
XX
PR 20-JUL-1992; 92US-00916901.
XX
PA (UYWA-) UNIV WAYNE STATE.
XX
PI Granneman JG, Lahners KN, Rao DD;
XX
DR WPI; 1994-048848/06.
DR P-PSDB; AAR45740.
XX
DT DNA encoding a beta 3-adrenergic receptor protein, opt. modified to avoid
DT fusion protein expression - can be used to identify cpds. which affect
DT receptor activity.
XX
CC Claim 4; Fig 1; 80pp; English.
XX
CC The human beta-3 adrenergic receptor protein is 408 amino acids long, not
CC 402 as previously reported, and is encoded as two introns. Host cells
CC expressing this DNA can be used to identify cpds. which affect the
CC activity of the receptor. Modifications in the DNA to mutate C1206 to T

protein. Oligonucleotide sequences which hybridise to this DNA may be used as probes to detect mRNA specific for beta-3 adrenergic receptor protein in cells. See also AAQ55694-707. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 1227 BP; 125 A; 465 C; 389 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 2; Length 1227;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
O        180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

Y         61 C 61
             |
O        240 C 240
```

RESULT 5
ADT93441
ADT93441 standard; DNA; 1227 BP.

ADT93441;

13-JAN-2005 (first entry)

Human beta3 adrenaline receptor (B3AR) T190 variant DNA.

single nucleotide polymorphism; SNP; SNP detection;
beta3 adrenaline receptor; ds.

Homo sapiens.

Key	Location/Qualifiers
variation	replace(190,C)
	/*tag= a
	/standard_name= "Single nucleotide polymorphism"

WO2004092385-A1.

28-OCT-2004.

16-APR-2004; 2004WO-JP005525.

18-APR-2003; 2003JP-00114381.

(ARKR-) ARKRAY INC.

Hirai M;

WPI; 2004-784610/77.

Nucleic acid probe useful for detecting mutation in beta3 adrenaline receptor gene having single nucleotide polymorphism, labeled at terminal with fluorescent dye and shows decrease in fluorescence of fluorescent dye upon hybridization.

Claim 1; SEQ ID NO 1; 31pp; Japanese.

The invention relates to a novel nucleic acid probe which is labelled at a terminal with a fluorescent dye, whereby a decrease in the fluorescence of the fluorescent dye is observed upon hybridisation. The probe comprises a base sequence derived from a fully defined sequence of 1227 nucleotides as given in the specification and being labelled at the 3' or 5' end with a fluorescent dye. The probe of the invention may be useful for detecting a mutation or single nucleotide polymorphism (SNP) in the beta3 adrenaline receptor (B3AR) gene. The probe is effective in detecting a B3AR Trp64Arg mutation within a short time whilst risk of

C contamination of the amplified product is prevented and the process is
C automated. The current sequence is that of the human beta3 adrenaline
C receptor (B3AR) T190 variant DNA of the invention.
XX
SQ Sequence 1227 BP; 125 A; 463 C; 391 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 13; Length 1227;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

Qy         61 C 61
              |
Db        240 C 240
```

RESULT 6
ACA56586
ID ACA56586 standard; cDNA; 1270 BP.
XX
AC ACA56586;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1184.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1184; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia

immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=06500938B1

Sequence 1270 BP; 132 A; 484 C; 405 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 10; Length 1270;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D        217 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 276

Y         61 C 61
             |
D        277 C 277
```

RESULT 7
DI56382
ID ADI56382 standard; DNA; 1270 BP.
XX
AC ADI56382;
XX
DT 22-APR-2004 (first entry)
XX
DE Human polynucleotide probe #1184.
XX
KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland; bladder; bone;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS Homo sapiens.
XX
PN US2004010136-A1.
XX
PD 15-JAN-2004.
XX
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2004-090520/09.
XX
PT New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
PS Claim 6; SEQ ID NO 1184; 73pp; English.
XX
CC The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the

diagnosis and treatment of cancer, an immunopathology or a
neuropathology. It can also be used for drug discovery and development,
toxicological and carcinogenicity studies, forensics or pharmacogenomics.
Microarrays can also be used for monitoring the progression of diseases
that may be associated with the altered expression of signalling pathway
polypeptides. The composition can also be used to purify a subpopulation
of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
is also useful for the diagnosis and treatment of cancer, e.g. cancers of
the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
epilepsy, Alzheimer's disease or depression. This sequence represents a
human polynucleotide probe of the invention. Note: The sequence data for
this patent did not form part of the printed specification but was
obtained in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html.

Sequence 1270 BP; 132 A; 484 C; 405 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 12; Length 1270;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o        217 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 276

y         61 C 61
             |
o        277 C 277
```

RESULT 8
AAQ05731
AAQ05731 standard; DNA; 2022 BP.

AAQ05731;

25-MAR-2003 (revised)
07-JAN-1991 (first entry)

Beta 3 adrenergic receptor gene.

Beta 3 adrenergic receptor gene; lipolysis; insulin; drugscreening; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	638. .1844
	/*tag= a
	/product= "beta 3 adrenergic receptor"

WO9008775-A.

09-AUG-1990.

25-JAN-1989; 89FR-00000918.

25-JAN-1989; 89FR-00000918.

(CNRS) CNRS CENT NAT RECH SCI.
(INSP) INST PASTEUR.

Emorine L, Rullo S, Strosberg D;

WPI; 1990-260892/34.
P-PSDB; AAR06495.

New beta 3 adrenergic receptor polypeptide and encoding nucleic acid -
involved in lipolysis, insulin secretion, etc. useful for screening drugs
to control these processes

S Disclosure; Fig 1bis; 51pp; French.
X
C The gene has been identified in a human genomic bank by screening with
C (a) the gene for turkey beta 1 receptor and (b) the gene for human beta 2
C receptor. Clones contg. an intron-free gene with better than 40% homology
C with the beta 1/2 genes were found and designated beta 3 receptor.
C Vectors for expression of this gene are plasmids, cosmids or phages, esp.
C the phage M13mp18-Hubeta3 (CNCM I-883), and these are used to transform
C bacteria or eukaryotic cells. The peptide is implicated in the lipolytic
C response of adipose tissue, in insulin secretion and in intestinal
C relaxation. It is useful for screening compunds which can act as specific
C ligands, i.e. potentially suitable as drugs for treatment of obesity,
C diabetes and hyperlipidaemia. (Updated on 25-MAR-2003 to correct PA
C field.)
X
S Sequence 2022 BP; 282 A; 679 C; 644 G; 414 T; 0 U; 3 Other;

Query Match   100.0%; Score 61; DB 2; Length 2022;
Best Local Similarity   100.0%; Pred. No. 1.3e-12;
Matches   61; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 876

Qy   61 C 61
              |
Db   877 C 877

RESULT 9
AAV23500
ID AAV23500 standard; cDNA; 2518 BP.
XX
AC AAV23500;
XX
DT 28-JUL-1998 (first entry)
XX
DE Human adrenaline beta-receptor nucleotide sequence.
XX
KW Human adrenilin beta-receptor; uncoupling protein; UCP; adipocyte;
KW metabolism; obesity; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   102. .1329
FT   /*tag= a
FT   /product= "human adrenaline beta-receptor product"
XX
PN JP10033178-A.
XX
PD 10-FEB-1998.
XX
PF 23-JUL-1996;   96JP-00193537.
XX
PR 23-JUL-1996;   96JP-00193537.
XX
PA (KAOS) KAO CORP.
XX
DR WPI; 1998-172096/16.
DR P-PSDB; AAW53847.
XX
PT Preparing cultured cells capable of converting into adypocytes - by
PT transferring cells with human adrenalin beta receptor and un-coupling
PT protein.
XX
PS Example 1; Fig 1; 8pp; Japanese.
XX
CC This is the nucleotide sequence for the human adrenilin beta receptor. In

C the presence of the uncoupling protein (UCP), capable of differentiating
C or converting into adipocytes. The cells may be used for the analysis of
C intracellular information transfer and energy metabolism, and development
C of compositions for the analysis and control of these systems. The cells
C can also be used for the prevention and treatment of obesity
K
D Sequence 2518 BP; 393 A; 824 C; 699 G; 602 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 2; Length 2518;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D 282 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 341

Y 61 C 61
|
D 342 C 342

ESULT 10
3Z42630
D ABZ42630 standard; DNA; 2644 BP.
K
C ABZ42630;
K
I 04-MAR-2003 (first entry)
K
E Human beta-3 adrenoceptor nucleotide SEQ ID NO:53.
K
W G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
W G protein-coupled receptor modulator; antibody; immune-related disease;
W growth-related disease; cell regeneration-related disease; AIDS; cancer;
W immunological-related cell proliferative disease; autoimmune disease;
W Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
W osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
W graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
W psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
W mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
W hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
W ulcer; gene; ds.
K
S Homo sapiens.
K
N WO200261087-A2.
K
D 08-AUG-2002.
K
F 19-DEC-2001; 2001WO-US050107.
K
R 19-DEC-2000; 2000US-0257144P.
K
A (LIFE-) LIFESPAN BIOSCIENCES INC.
K
I Burmer GC, Roush CL, Brown JP;
K
R WPI; 2003-046718/04.
R P-PSDB; ABP81786.
K
T New isolated antigenic peptides e.g., for G protein-coupled receptors
T (GPCR), useful for diagnosing and designing drugs for treating conditions
T in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
T autoimmune diseases.
K
S Disclosure; Fig 1; 523pp; English.
K
C The present invention describes antigenic peptides (I) comprising: (a)
C any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
C acids. Also described: (1) an assay for the detection of a particular G
C protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

C and (2) an isolated antibody having high specificity and high affinity of
C avidity for a particular GPCR. (I) can be used as GPCR modulators and in
C gene therapy. The antigenic peptides for GPCRs are useful in detecting an
C antibody against a particular GPCR, and in the production of specific
C antibodies. The peptides and antibodies are also useful for detecting the
C presence or absence of corresponding GPCRs. The antigenic peptides for
C GPCRs and antibodies are useful for diagnosing and designing drugs for
C treating immune-related diseases, growth-related diseases, cell
C regeneration-related disease, immunological-related cell proliferative
C diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
C atherosclerosis, bacterial, fungal, protozoan or viral infections,
C osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
C inflammation, allergies, Crohn's disease, diabetes, graft versus host
C disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
C anxiety, depression, schizophrenia, dementia, mental retardation, memory
C loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
C hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
C any other disorder in which GPCRs are involved. The antibodies may be
C used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
C GPCR proteins given in ABP81675 to ABP82018, which are used in the
C exemplification of the present invention
XX
SQ Sequence 2644 BP; 422 A; 856 C; 741 G; 625 T; 0 U; 0 Other;

 Query Match   100.0%; Score 61; DB 8; Length 2644;
 Best Local Similarity   100.0%; Pred. No. 1.4e-12;
 Matches   61; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   377 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 436

Qy   61 C 61
              |
Db   437 C 437

RESULT 11
ADN39372
ID   ADN39372 standard; cDNA; 2644 BP.
XX
AC   ADN39372;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B56.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.

R 20-FEB-2002; 2002US-0359077P.
R 29-MAR-2002; 2002US-0368809P.
R 04-APR-2002; 2002US-0370110P.
R 12-APR-2002; 2002US-0372246P.
R 05-JUN-2002; 2002US-0386614P.
R 16-JUL-2002; 2002US-0396839P.
R 22-JUL-2002; 2002US-0397775P.
R 22-JUL-2002; 2002US-0397845P.
R 09-SEP-2002; 2002US-0409450P.
X
A (EOSB-) EOS BIOTECHNOLOGY INC.
X
I Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
I Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
X
R WPI; 2003-468649/44.
R P-PSDB; ADN39373.
X
T Determining the presence or absence of a pathological cell in a patient,
T useful for diagnosing, prognosing or treating cancer, comprises detecting
T a nucleic acid in a biological sample.
X
S Claim 8; SEQ ID NO B56; 1385pp; English.
X
C The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
C whose expression is upregulated or downregulated in specific cancers or
C other diseases such as angiogenic or fibrotic disorders, and to methods
C of determining the presence or absence of a pathological cell in a
C patient by detecting a nucleic acid at least 80% identical to those of
C the invention or by detecting a polypeptide of the invention. The
C invention also relates to expression vectors and host cells comprising a
C nucleic acid of the invention; antibodies which specifically bind a
C polypeptide of the invention; use of such antibodies for drug targeting;
C and methods of screening for modulators of activity or expression of the
C polypeptides and nucleic acids. The nucleic acids, polypeptides,
C antibodies and methods are useful for diagnosing, prognosing and treating
C cancer and other conditions such as psoriasis, ischaemia, heart disease,
C atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
C neovascularistaion syndromes, scarring and uterine fibroids. They may
C also be useful in wound healing and in contraception. The present
C sequence represents a nucleic acid sequence of the invention.
X
Q Sequence 2644 BP; 422 A; 856 C; 741 G; 625 T; 0 U; 0 Other;

Query Match 100.0%; Score 61; DB 11; Length 2644;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o 377 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 436

Y 61 C 61
   |
o 437 C 437

ESULT 12
DO29809
D ADO29809 standard; cDNA; 2644 BP.
X
C ADO29809;
X
T 29-JUL-2004 (first entry)
X
E Human GPCR ADRB3 polynucleotide, SEQ ID NO:911.
X
W G protein-coupled receptor; GPCR; drug screening; diagnosis;
W transgenic mouse; neurological disorder; adrenal gland disorder;
W colon disorder; intestinal disorder; cardiovascular disorder;

WN joint disorder; metabolic disorder; nutritive disorder; cancer;
WN kidney disorder; liver disorder; lung disorder; breast disorder;
WN ovary disorder; uterus disorder; prostate disorder; testis disorder;
WN skin disorder; stomach disorder; pancreas disorder; spleen disorder;
WN thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
WN cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
WN CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
WN virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
WN dermatological; antiulcer; antithyroid; antiallergic; anorectic;
WN immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
WN gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX

SCORE Search Results Details for Application 10553509 and Search Result 20061214_104404_us-10-553-509-1_copy_180_240.rni.

his page gives you Search Results detail for the Application 10553509 and Search Result 20061214_104404_us-10-53-509-1_copy_180_240.rni.

tart

Go Back to previous pag

GenCore version 5.1.9

M nucleic - nucleic search, using sw model

un on: December 15, 2006, 15:53:11 ; Search time 152.186 Seconds
(without alignments)
749.990 Million cell updates/sec

itle: US-10-553-509-1_COPY_180_240
erfect score: 61
equence: 1 ggccatcgcctggactccga.....tgttcgtgacttcgctggcc 61

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 1403666 seqs, 935554401 residues

otal number of hits satisfying chosen parameters: 2807332

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	1134	2	US-08-087-772A-14	Sequence 14, Appl
2	61	100.0	1185	5	US-09-993-844A-13	Sequence 13, Appl
3	61	100.0	1227	2	US-07-916-901-1	Sequence 1, Appli
4	61	100.0	1227	2	US-08-351-473B-7	Sequence 7, Appli
5	61	100.0	1270	3	US-09-016-434-1184	Sequence 1184, Ap

	8	61	100.0	3683	3	US-09-895-211-1	Sequence 1, Appli
	9	57.8	94.8	1218	2	US-08-351-473B-6	Sequence 6, Appli
	10	57.8	94.8	2000	2	US-08-351-473B-1	Sequence 1, Appli
	11	50.4	82.6	298	2	US-08-087-772A-7	Sequence 7, Appli
	12	50.4	82.6	1164	2	US-08-087-772A-3	Sequence 3, Appli
	13	50.4	82.6	1360	2	US-08-087-772A-4	Sequence 4, Appli
	14	50.4	82.6	1920	2	US-08-087-772A-1	Sequence 1, Appli
	15	50.4	82.6	2005	2	US-07-916-901-5	Sequence 5, Appli
	16	50.4	82.6	3437	3	US-08-450-962-3	Sequence 3, Appli
	17	50.4	82.6	3437	3	US-08-848-631-3	Sequence 3, Appli
	18	50.4	82.6	3437	3	US-09-895-211-3	Sequence 3, Appli
	19	38.6	63.3	4749	3	US-09-614-034-189	Sequence 189, App
	20	37	60.7	1845	3	US-09-614-034-188	Sequence 188, App
	21	36	59.0	1584	3	US-09-614-034-194	Sequence 194, App
	22	35.4	58.0	1525	3	US-09-614-034-193	Sequence 193, App
	23	35.4	58.0	1723	3	US-09-614-034-187	Sequence 187, App
	24	35.4	58.0	1723	3	US-09-016-434-1182	Sequence 1182, Ap
	25	35.4	58.0	4401	3	US-09-614-034-192	Sequence 192, App
	26	28	45.9	1113	5	US-09-993-844A-9	Sequence 9, Appli
	27	28	45.9	1242	7	PCT-US91-00909-3	Sequence 3, Appli
	28	28	45.9	2305	3	US-09-016-434-1282	Sequence 1282, Ap
	29	28	45.9	2305	3	US-09-023-655-1249	Sequence 1249, Ap
	30	28	45.9	2340	3	US-09-856-803-1	Sequence 1, Appli
	31	28	45.9	3451	3	US-09-811-286-1	Sequence 1, Appli
	32	25.4	41.6	1254	7	PCT-US91-00909-1	Sequence 1, Appli
	33	24.6	40.3	29	3	US-09-304-232-896	Sequence 896, App
c	34	24	39.3	1368	3	US-09-906-408A-4	Sequence 4, Appli
	35	23.8	39.0	525	3	US-09-252-991A-14501	Sequence 14501, A
	36	23.8	39.0	903	3	US-09-252-991A-10886	Sequence 10886, A
	37	23.8	39.0	1035	4	US-10-324-967-11	Sequence 11, Appl
	38	23.8	39.0	1092	3	US-09-252-991A-14759	Sequence 14759, A
	39	23.8	39.0	1158	3	US-09-252-991A-10906	Sequence 10906, A
c	40	23.8	39.0	1305	3	US-09-252-991A-10830	Sequence 10830, A
	41	23.8	39.0	2145	3	US-09-252-991A-14638	Sequence 14638, A
c	42	23.8	39.0	2487	3	US-09-252-991A-14985	Sequence 14985, A
c	43	23.8	39.0	3450	3	US-09-902-540-9001	Sequence 9001, Ap
	44	23.8	39.0	7305	3	US-09-902-540-961	Sequence 961, App
c	45	23.4	38.4	1242	3	US-09-489-039A-5521	Sequence 5521, Ap

ALIGNMENTS

ESULT 1
3-08-087-772A-14
Sequence 14, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800

NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1134 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-087-772A-14

Query Match 100.0%; Score 61; DB 2; Length 1134;
Best Local Similarity 100.0%; Pred. No. 7.9e-13;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o 180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

y 61 C 61
|
o 240 C 240

ESULT 2
3-09-993-844A-13
Sequence 13, Application US/09993844A
Patent No. 7018812
GENERAL INFORMATION:
APPLICANT: Oakley, Robert H.
APPLICANT: Barak, Lawrence S.
APPLICANT: Laporte, Stephane A.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Modified G-Protein Coupled Receptors
FILE REFERENCE: 033072-026
CURRENT APPLICATION NUMBER: US/09/993,844A
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/260,363
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1185
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotide sequence of beta3-AR-V2R chimera
3-09-993-844A-13

Query Match 100.0%; Score 61; DB 5; Length 1185;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o 180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

y 61 C 61
|
o 240 C 240

ESULT 3
3-07-916-801-1

Sequence 1, Application US/07916901
Patent No. 5364772
GENERAL INFORMATION:
APPLICANT: Granneman, James G.
APPLICANT: Lahners, Kristine N.
APPLICANT: Rao, Donald D.
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
ADDRESSEE: MILTON
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: USA
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,901
FILING DATE: 19920720
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324(WSU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1224
3-07-916-901-1

Query Match 100.0%; Score 61; DB 2; Length 1227;
Best Local Similarity 100.0%; Pred. No. 8.1e-13;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D        180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

Y         61 C 61
             |
D        240 C 240
```

ESULT 4
3-08-351-473B-7
Sequence 7, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-351-473B-7

Query Match 100.0%; Score 61; DB 2; Length 1227;
Best Local Similarity 100.0%; Pred. No. 8.1e-13;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D 180 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

Y 61 C 61
|
D 240 C 240

ESULT 5
3-09-016-434-1184
Sequence 1184, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,191
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1184:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g178895
3-09-016-434-1184

Query Match 100.0%; Score 61; DB 3; Length 1270;
Best Local Similarity 100.0%; Pred. No. 8.1e-13;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o 217 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 276

y 61 C 61
|
o 277 C 277

ESULT 6
3-08-450-962-1
Sequence 1, Application US/08450962
Patent No. 6274706
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROSBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR89/00918

FILING DATE: 25 JAN 1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3683 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
3-08-450-962-1

Query Match 100.0%; Score 61; DB 3; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o 817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 876

y 61 C 61
|
o 877 C 877

ESULT 7
3-08-848-631-1
Sequence 1, Application US/08848631
Patent No. 6635442
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
STROSBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
MOUSE a3-ADRENERGIC RECEPTOR
GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,631
FILING DATE: 08-Jun-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3683 bases
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
3-08-848-631-1

Query Match 100.0%; Score 61; DB 3; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o        817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 876

Y         61 C 61
             |
o        877 C 877
```

ESULT 8
3-09-895-211-1
Sequence 1, Application US/09895211
Patent No. 6949636
GENERAL INFORMATION:
APPLICANT: Hunton and Williams
APPLICANT: Emorine, Laurent
TITLE OF INVENTION: INTRON/EXON STRUCTURE OF THE HUMAN AND MOUSE BETA3 ADRENERGIC RECEPTOR
TITLE OF INVENTION: GENES
FILE REFERENCE: 58769.000011
CURRENT APPLICATION NUMBER: US/09/895,211
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 3683
TYPE: DNA
ORGANISM: Homo sapiens
3-09-895-211-1

Query Match 100.0%; Score 61; DB 3; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Y          1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o        817 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 876

Y         61 C 61
             |
o        877 C 877
```

ESULT 9
3-08-351-473B-6
Sequence 6, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-351-473B-6

Query Match 94.8%; Score 57.8; DB 2; Length 1218;
Best Local Similarity 96.7%; Pred. No. 1.2e-11;
Matches 59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
o 180 GGCCATCGCCCGGACGCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 239

y 61 C 61
|
o 240 C 240

ESULT 10
3-08-351-473B-1
Sequence 1, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1321
OTHER INFORMATION: /function= "BOVINE BETA-3 RECEPTOR"
OTHER INFORMATION: /product= "ADRENERGIC, BETA RECEPTOR"
3-08-351-473B-1

Query Match 94.8%; Score 57.8; DB 2; Length 2000;
Best Local Similarity 96.7%; Pred. No. 1.4e-11;
Matches 59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1 GGCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 60
||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
o 286 GGCCATCGCCCGGACGCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGC 345

y 61 C 61
|
o 346 C 346

ESULT 11
3-08-087-772A-7
Sequence 7, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 881 3140

TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-087-772A-7

Query Match 82.6%; Score 50.4; DB 2; Length 298;
Best Local Similarity 90.0%; Pred. No. 4.6e-09;
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

y 2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCC 61
||||||||| | || |||||||| |||||||| |||||||||||||||||||| ||||||
o 173 GCCATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTCGTGACTTCACTGGCC 232

ESULT 12
3-08-087-772A-3
Sequence 3, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-087-772A-3

Query Match 82.6%; Score 50.4; DB 2; Length 1164;
Best Local Similarity 90.0%; Pred. No. 6.3e-09;
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

y 2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCC 61
||||||||| | || |||||||| |||||||| |||||||||||||||||||| ||||||
o 172 GCCATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTCGTGACTTCACTGGCC 231

3-08-087-772A-4
Sequence 4, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-087-772A-4

Query Match 82.6%; Score 50.4; DB 2; Length 1360;
Best Local Similarity 90.0%; Pred. No. 6.5e-09;
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

y 2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCC 61
||||||||| | || |||||||| |||||||| |||||||||||||||||||| ||||||
o 185 GCCATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTCGTGACTTCACTGGCC 244

ESULT 14
3-08-087-772A-1
Sequence 1, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 568..1731
3-08-087-772A-1

Query Match 82.6%; Score 50.4; DB 2; Length 1920;
Best Local Similarity 90.0%; Pred. No. 7.1e-09;
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Y 2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCC 61
||||||||| | || |||||||| |||||||| |||||||||||||||||||| ||||||
O 739 GCCATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTCGTGACTTCACTGGCC 798

ESULT 15
3-07-916-901-5
Sequence 5, Application US/07916901
Patent No. 5364772
GENERAL INFORMATION:
APPLICANT: Granneman, James G.
APPLICANT: Lahners, Kristine N.
APPLICANT: Rao, Donald D.
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
ADDRESSEE: MILTON
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: USA
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,901
FILING DATE: 19920720
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324(WSU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 5:

LENGTH: 2005 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1250
3-07-916-901-5

Query Match 82.6%; Score 50.4; DB 2; Length 2005;
Best Local Similarity 90.0%; Pred. No. 7.1e-09;
Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
y          2 GCCATCGCCTGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCC 61
             || |||||| | || |||||||| |||||||| ||||||||||||||||||||||||||
o        222 GCTATCGCCCGCACGCCGAGACTACAGACCATAACCAACGTGTTCGTGACTTCGCTGGCC 281
```

earch completed: December 15, 2006, 18:01:34
ob time : 154.186 secs

tart